

BLASTN 2.2.19+

Reference: Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.

RID: URU3KT33016

Database: Nucleotide sequences derived from the Patent division of GenBank

8,753,385 sequences; 4,832,233,817 total letters

Query= SID_3

Length=2660

Sequences producing significant alignments:	Score (Bits)	E Value
dbj DI129697.1 AN EXPRESSION CASSETTE AND VECTOR FOR TRANSIENT EXPRESSION	4817	0.0
dbj DI109112.1 FLP-mediated Recombination	4817	0.0
dbj DJ052243.1 FLP-mediated Recombination	4817	0.0
dbj DD418156.1 AN EXPRESSION CASSETTE AND VECTOR FOR TRANSIENT EXPRESSION	4817	0.0
dbj E00140.1 Genomic DNA encoding human growth hormone	4795	0.0
emb AX719120.1 Sequence 1 from Patent EP1295938	4724	0.0
emb AX659146.1 Sequence 1 from Patent WO20101002	4724	0.0
emb CS741886.1 Sequence 9882 from Patent WO2005083127	4684	0.0
emb CS741885.1 Sequence 9881 from Patent WO2005083127	4684	0.0
gb GC699295.1 Sequence 14540 from patent US 6812339	2802	0.0
gb GC699294.1 Sequence 14539 from patent US 6812339	2802	0.0
gb GC699293.1 Sequence 14538 from patent US 6812339	2802	0.0
gb GC699292.1 Sequence 14537 from patent US 6812339	2802	0.0
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gb GC699290.1 Sequence 14535 from patent US 6812339	2802	0.0
gb GC699289.1 Sequence 14534 from patent US 6812339	2802	0.0
gb GC699288.1 Sequence 14533 from patent US 6812339	2802	0.0
gb GC699287.1 Sequence 14532 from patent US 6812339	2802	0.0
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gb GC699282.1 Sequence 14527 from patent US 6812339	2802	0.0
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gb GC699279.1 Sequence 14524 from patent US 6812339	2802	0.0
gb GC699278.1 Sequence 14523 from patent US 6812339	2802	0.0
gb GC699277.1 Sequence 14522 from patent US 6812339	2802	0.0
gb GC699276.1 Sequence 14521 from patent US 6812339	2802	0.0
emb FB669399.1 Sequence 44 from Patent WO2007144105	2796	0.0
dbj DI131946.1 Growth Hormone Variation in Humans and its uses	2796	0.0
emb CS694111.1 Sequence 25 from Patent WO2007077422	2796	0.0
emb CS694086.1 Sequence 7 from Patent WO2007077423	2796	0.0
dbj DD441736.1 Growth Hormone Variation in Humans and its uses	2796	0.0
dbj DD211379.1 New Mutations	2796	0.0
emb CQ818162.1 Sequence 1 from Patent WO2004044002	2796	0.0
emb AX767318.1 Sequence 1 from Patent WO03042245	2796	0.0
emb AX512768.1 Sequence 2 from Patent EP1233063	2793	0.0
dbj DD164250.1 Single Nucleotide Polymorphisms in GH-1	2776	0.0
gb I41411.1 I41411 Sequence 5 from patent US 5625124	2702	0.0
gb AR134712.1 AR134712 Sequence 9 from patent US 6194176	2625	0.0

gb AR108064.1 AR108064	Sequence 9 from patent US 6110707	2625	0.0
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dbj DI105645.1	Expression system	2135	0.0
dbj DD292520.1	GENE EXPRESSION SYSTEM BASED ON CODON TRANSLA...	2135	0.0
dbj DI013548.1	PHAGE-DEPENDENT SUPER PRODUCTION OF BIOLOGICA...	2102	0.0
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gb AR575651.1	Sequence 8 from patent US 6773899	2102	0.0
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emb CS704166.1	Sequence 2473 from Patent WO2006081249	2091	0.0
gb AR119909.1 AR119909	Sequence 1 from patent US 6153427	2091	0.0
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dbj DI105163.1	Expression system	1969	0.0
dbj DD292521.1	GENE EXPRESSION SYSTEM BASED ON CODON TRANSLA...	1969	0.0
dbj DD373892.1	METHODS FOR DIAGNOSING RCC AND OTHER SOLID TU...	1923	0.0
emb CS732094.1	Sequence 90 from Patent WO2005083127	1797	0.0
gb AR108119.1 AR108119	Sequence 72 from patent US 6110707	1731	0.0
gb AR108118.1 AR108118	Sequence 70 from patent US 6110707	1731	0.0
gb IO2855.1	Sequence 1 from Patent US 4446235	1511	0.0
gb IO2856.1	Sequence 2 from Patent US 4446235	1339	0.0
dbj DL066432.1	Cancer Gene Determination and Therapeutic Scr...	1308	0.0
emb AX335036.1	Sequence 5545 from Patent WO0194629	1308	0.0
emb CS732112.1	Sequence 108 from Patent WO2005083127	1301	0.0
emb CS732114.1	Sequence 110 from Patent WO2005083127	1242	0.0
emb CS732113.1	Sequence 109 from Patent WO2005083127	1238	0.0
emb CS732104.1	Sequence 100 from Patent WO2005083127	1238	0.0
emb CS732100.1	Sequence 96 from Patent WO2005083127	1238	0.0
emb CS732095.1	Sequence 91 from Patent WO2005083127	1238	0.0
emb CS732086.1	Sequence 82 from Patent WO2005083127	1238	0.0
emb CS732111.1	Sequence 107 from Patent WO2005083127	1236	0.0
emb CS732093.1	Sequence 89 from Patent WO2005083127	1236	0.0
emb CS732092.1	Sequence 88 from Patent WO2005083127	1234	0.0
dbj DI012300.1	METHODS OF TREATMENT USING Erbb ANTIBODY-MAYT...	1227	0.0
gb AR928865.1	Sequence 7 from patent US 7097840	1227	0.0
gb AR409602.1	Sequence 1 from patent US 6632979	1227	0.0
emb AX060703.1	Sequence 1 from Patent WO0100244	1227	0.0
gb IO2857.1	Sequence 3 from Patent US 4446235	1227	0.0
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emb CS457474.1	Sequence 3 from Patent EP1731607	1168	0.0
emb CQ803124.1	Sequence 10 from Patent WO2004035782	1168	0.0
emb CQ803123.1	Sequence 9 from Patent WO2004035782	1168	0.0
emb CQ803122.1	Sequence 8 from Patent WO2004035782	1168	0.0
emb CQ803121.1	Sequence 7 from Patent WO2004035782	1168	0.0
emb CQ803120.1	Sequence 6 from Patent WO2004035782	1168	0.0
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gb GC693420.1	Sequence 2793 from patent US 6812339	1109	0.0
gb GC693419.1	Sequence 2792 from patent US 6812339	1109	0.0
gb GC693418.1	Sequence 2791 from patent US 6812339	1109	0.0
gb GC693417.1	Sequence 2790 from patent US 6812339	1109	0.0
gb GC693416.1	Sequence 2789 from patent US 6812339	1109	0.0
dbj DI126066.1	AN EXPRESSION CASSETTE AND VECTOR FORTRANSIEN...	1098	0.0
dbj DD418157.1	AN EXPRESSION CASSETTE AND VECTOR FOR TRANSIE...	1098	0.0
dbj DJ418990.1	Methods And Constructs For Expressing Polypep...	1068	0.0
dbj DI151081.1	Methods And Constructs For Expressing Polypep...	1068	0.0
dbj DI128841.1	AN EXPRESSION CASSETTE AND VECTOR FORTRANSIEN...	1068	0.0
dbj DD418139.1	AN EXPRESSION CASSETTE AND VECTOR FOR TRANSIE...	1068	0.0
emb CS732108.1	Sequence 104 from Patent WO2005083127	1033	0.0
emb CS732101.1	Sequence 97 from Patent WO2005083127	1033	0.0

ALIGNMENTS

>obj|D1129697.1| AN EXPRESSION CASSETTE AND VECTOR FOR TRANSIENT OR STABLE EXPRESSION OF EXOGENOUS MOLECULES
Length=2660

Score = 4817 bits (2608), Expect = 0.0
Identities = 2660/2660 (100%), Gaps = 0/2660 (0%)
Strand=Plus/Plus

Query 1	GAATTCACTGAATCATGCCAGAACCCCCGCAATCTATTGGCTGTGCTTGGCCCT	60
Sbjct 1	GAATTCACTGAATCATGCCAGAACCCCCGCAATCTATTGGCTGTGCTTGGCCCT	60
Query 61	TTCCTTAAACACACACATCTCTCTGGTGGGGAGGGAAACATGGGGGAGGAGGAAG	120
Sbjct 61	TTCCTTAAACACACACACATCTCTCTGGTGGGGAGGGAAACATGGGGGAGGAGGAAG	120
Query 121	GAATAGGATAGAGAGTGGATGGGTGGTCTGGTAGGGTCTCAAGGACTGGCTATCTGACA	180
Sbjct 121	GAATAGGATAGAGAGTGGATGGGTGGTCTGGTAGGGTCTCAAGGACTGGCTATCTGACA	180
Query 181	TCTCTCTCCCGCTTCAGGTTGGGACCATGGCTGCTGCCAGAGGGCACCCACGTGACCC	240
Sbjct 181	TCTCTCTCCCGCTTCAGGTTGGGACCATGGCTGCTGCCAGAGGGCACCCACGTGACCC	240
Query 241	TTAAAGAGAGGACAAGTGGGGTGTATCTCTGGCTGACATTCTGTGACAACCCTCACAA	300
Sbjct 241	TTAAAGAGAGGACAAGTGGGGTGTATCTCTGGCTGACATTCTGTGACAACCCTCACAA	300
Query 301	CGCTGGTGATGGTGGGAAGGGAAAGATGACAAGTCAGGGGCATGATCCCAGCATGTG	360
Sbjct 301	CGCTGGTGATGGTGGGAAGGGAAAGATGACAAGTCAGGGGCATGATCCCAGCATGTG	360
Query 361	GGAGGAGCTCTAAATTATCATTAGCACAAGCCCGTCAGTGGCCCCAGGCCCTAAACATG	420
Sbjct 361	GGAGGAGCTCTAAATTATCATTAGCACAAGCCCGTCAGTGGCCCCAGGCCCTAAACATG	420
Query 421	CAGAGAACAGGTGAGGAGAACGACGGAGAGAGAACGGGCCAGTATAAAAGGGCCAC	480
Sbjct 421	CAGAGAACAGGTGAGGAGAACGACGGAGAGAACGGGCCAGTATAAAAGGGCCAC	480
Query 481	AAGAGACCAGCTAAGGATCCAAAGGCCAACTCCCCGAACCACTCAGGGTCTGTGGAC	540
Sbjct 481	AAGAGACCAGCTAAGGATCCAAAGGCCAACTCCCCGAACCACTCAGGGTCTGTGGAC	540
Query 541	AGCTCACTAGCGGAATGGCTGCAGGTAAAGGCCCTAAATCCCTTGGCACAATGTGT	600
Sbjct 541	AGCTCACTAGCGGAATGGCTGCAGGTAAAGGCCCTAAATCCCTTGGCACAATGTGT	600
Query 601	CCTGAGGGAGAGGCCGGCTCTGTAGATGGGACGGGGCACTAACCTCAGGTTGGG	660
Sbjct 601	CCTGAGGGAGAGGCCGGCTCTGTAGATGGGACGGGGCACTAACCTCAGGTTGGG	660
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Sbjct 661	CTTATGAATGTTAGCTATGCCATCTAACGCCAGTATGGCAATCTGTGAATGTTCC	720
Query 721	GGTCCCTGGAGGGAGGAG	780
Sbjct 721	GGTCCCTGGAGGGAGGAG	780

Query	781	GAGAGCGCTGGCCCTTGCCTCCAGCTCCCTCTGGCTCCGGTTCTCCCAAGGCTC	840
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Query	841	CCGGACGTCCCTGCTCTGGCTTTGGCTGCTCTGCCGTCTGGCTCAAGAGGGCAG	900
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Sbjct	901	TGCCTCCCAACCATTCCCTATCCAGGTTTGTACAACGCTATGCTCCGCCGTCG	960
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Sbjct	1021	GCTTCAGAGGTGGCAGGAAGGGTGAAATTCCCCGCTGGAGTAATGGGAGGAGACTA	1080
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Sbjct	1081	AGGAGCTCAGGGTTGTTCTGAAGTGAAAATGCAGGAGATGAGCATACGCTGAGTGAG	1140
Query	1141	GTTCCAGAAAAGTAACAATGGAGCAGGTCTCCAGCATAGACCTTGGTGGCGGTCTT	1200
Sbjct	1141	GTTCCAGAAAAGTAACAATGGAGCAGGTCTCCAGCATAGACCTTGGTGGCGGTCTT	1200
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Sbjct	1201	CTCCTAGGAAGAACCTATACCTGAAGGAGCAGAAGTATTCTGCAGAACCCCA	1260
Query	1261	GACCTCCCTCTGCTCTCAGAGTCTATTCAACACCTTCCAACAGGGTGAAAACGCAGCA	1320
Sbjct	1261	GACCTCCCTCTGCTCTCAGAGTCTATTCAACACCTTCCAACAGGGTGAAAACGCAGCA	1320
Query	1321	GAAACTGTGAGGTGGATGCCCTCTCCCAAGGTGGATGGGTAGACCTGTGGTCAGAGCC	1380
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Query	1381	CCCGGGCAGCACAGCCACTGCCGTCTCCCTGCAGAACCTAGAGCTGCCATCT	1440
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Query	1501	ACAGCCTGGGTGATGGCGCTCGGACAGCAACGCTATGCCACCTGAAGGACCTAGAGG	1560
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Query	1681	CCCAAGAGAACTCACCGTATTCTCATTTCCCTCGTAATCCTCCAGGCCTTCTAC	1740
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Query	1861	GGGCAGATCTCAATCAGTCTCACAGCAAGTTGACACAAAATCGCACACAGTGACGCA	1920
Sbjct	1861	GGGCAGATCTCAATCAGTCTCACAGCAAGTTGACACAAAATCGCACACAGTGACGCA	1920
Query	1921	CTGCTCAAGRACTACGGGCTGCTACTGCTCAGGAAGGACATGGACAAGGTCGAGACA	1980
Sbjct	1921	CTGCTCAAGRACTACGGGCTGCTACTGCTCAGGAAGGACATGGACAAGGTCGAGACA	1980
Query	1981	TTCCCTGCGCATCGTGCAGTGCCTCTGTGGAGGGCAGCTGTGGCTTAGCTGCCCGG	2040
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Query	2041	TGGCATCCCCTGTGACCCCTCCCCAGTGCCCTCTCGCTGTGGAGGGCAGCTGTGGCTTAGCTGCCAGTG	2100
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Query	2101	CCCACCACTGTCTAATAAAATTAGTTGCATCATTTGTTGACTAGGTGTCTTG	2160
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Sbjct	2161	TATAATATTATGGGTGGAGGCCGGTGGTATGGAGCAAGGGGCCAGGTTGGAAAGACAAC	2220
Query	2221	CTGTAGGGCTTCAAGGTCTATTGGAAACAGGTGGAGTGGCAGTGGCAGTCTGGCT	2280
Sbjct	2221	CTGTAGGGCTTCAAGGTCTATTGGAAACAGGTGGAGTGGCAGTGGCAGTCTGGCT	2280
Query	2281	GCTGCAATCTCCGCTCTGGGTCAGCGATTCTCTGCCTCAGTCTCCGAATAGTTG	2340
Sbjct	2281	GCTGCAATCTCCGCTCTGGGTCAGCGATTCTCTGCCTCAGTCTCCGAATAGTTG	2340
Query	2341	CGATTCCAGGCATGCAAGACCAAGGCTCAGCTAATTTTGATTTGGTAGAGACGGGGT	2400
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Query	2401	TTCACCATATTGGCAGTCTGGTCTCCATCTCTGACCTCAGGTAATCCGCCCGCTCGG	2460
Sbjct	2401	TTCACCATATTGGCAGTCTGGTCTCCATCTCTGACCTCAGGTAATCCGCCCGCTCGG	2460
Query	2461	CCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTCCCTGCTCTGTGATT	2520
Sbjct	2461	CCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTCCCTGCTCTGTGATT	2520
Query	2521	TAAAAATAATTACACAGCAGAAGGACGTCCAGACACAGCATGGCTACCTGGCATGCC	2580
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Query 2581 AGCCAGTTGGACATTGAGTTGCTTGCCTGGCAGTCCTCTCATGCATTGGTCAC 2640
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Sbjct 2581 AGCCAGTTGGACATTGAGTTGCTTGCCTGGCAGTCCTCTCATGCATTGGTCAC 2640
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Query 2641 AGTAGATGCTTGTGAATT 2660
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Sbjct 2641 AGTAGATGCTTGTGAATT 2660

>dbj|DI109112.1| FLP-mediated Recombination
Length=2660

Score = 4817 bits (2608), Expect = 0.0
Identities = 2660/2660 (100%), Gaps = 0/2660 (0%)
Strand=Plus/Plus

Query 1 GAATTCACTGAATCATGCCAGAACCCCCGCAATCTATTGGCTGTGCTTGGCCCT 60
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Sbjct 1 GAATTCACTGAATCATGCCAGAACCCCCGCAATCTATTGGCTGTGCTTGGCCCT 60
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Query 61 TTCCCCAACACACACATTCTGTCTGGTGGGGAGGGAAACATGCGGGGAGGAGGAAG 120
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Sbjct 241 TTAAAGAGAGGACAAGTTGGGTGTATCTCTGGCTGACATTCTGTGACAACCCCTACAA 300
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Query 301 CGCTGGTGTGGTGGAAAGGGAAAGATGACAAGTCAGGGGGCATGATCCAGCATGTG 360
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Query 481 AAGAGACCCTCAAGGATCCAAAGGCCAACCTCCGAACCACTCAGGGTCCCTGTGGAC 540
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Sbjct 481 AAGAGACCCTCAAGGATCCAAAGGCCAACCTCCGAACCACTCAGGGTCCCTGTGGAC 540
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Query 541 AGCTCACTAGCGCAATGGCTGCAGTAAGGCCCTAAATCCCTTGGCACAATGTGT 600
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Query 661	CTTATGAATGTTAGCTATCGCCATCTAACGCCAGTATTGGCCAATCTCTGAATGTTCT	720
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Query 721	GGTCCCCTGGAGGGAGGAGagagagagagagaaaaaaaCCCAGCTCTGGAAACAGG	780
Sbjct 721	GGTCCCCTGGAGGGAGGAGAGAGAGAGAGAGAAAAAAACCCAGCTCTGGAAACAGG	780
Query 781	GAGAGCGCTGGGCCTTGTCTCCAGCTCCCTGTGCTCCAGCTCCCTGTGCTCCGGTTCTCCCCAGGCTC	840
Sbjct 781	GAGAGCGCTGGGCCTTGTCTCCAGCTCCCTGTGCTCCAGCTCCCTGTGCTCCGGTTCTCCCCAGGCTC	840
Query 841	CCGGACGTCCCCTGTCTGGCTTGGCTCTGGCTCTGGCTCTGGCTTCAGAGGGCAG	900
Sbjct 841	CCGGACGTCCCCTGTCTGGCTTGGCTCTGGCTCTGGCTCTGGCTTCAGAGGGCAG	900
Query 901	TGCTTCCCAACCATTCCCTATCCAGGCTTTGACAACGCTATGCTCCGCGCCGTC	960
Sbjct 901	TGCTTCCCAACCATTCCCTATCCAGGCTTTGACAACGCTATGCTCCGCGCCGTC	960
Query 961	CCTGTACCGCTGGCATATGACACCTATCAGGAGTTGTAAGCTTGGTAATGGTGC	1020
Sbjct 961	CCTGTACCGCTGGCATATGACACCTATCAGGAGTTGTAAGCTTGGTAATGGTGC	1020
Query 1021	GCTTCAGAGGTGGCAGGAAGGGGTGAATTCCCCCGCTGGGAAGTAATGGGAGGAGACTA	1080
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Query 1081	AGGAGCTCAGGGTTGTTCTGAAGTAAAATGCAGGCAGATGAGCATACTGCTGAGTGAG	1140
Sbjct 1081	AGGAGCTCAGGGTTGTTCTGAAGTAAAATGCAGGCAGATGAGCATACTGCTGAGTGAG	1140
Query 1141	GTTCCCAGAAAAGTAACATGGGAGCAGGTCTCCAGCATAGACCTTGGTGGCGGTCTT	1200
Sbjct 1141	GTTCCCAGAAAAGTAACATGGGAGCAGGTCTCCAGCATAGACCTTGGTGGCGGTCTT	1200
Query 1201	CTCTCTAGGAAGAACGCTATATCCTGAAGGAGCAGGAAGTATTCTGCAGAACCCCCA	1260
Sbjct 1201	CTCTCTAGGAAGAACGCTATATCCTGAAGGAGCAGGAAGTATTCTGCAGAACCCCCA	1260
Query 1261	GACCTCCCTGCTCTCAGAGCTATTCAACACCTTCAACAGGGTGAAAACGCAGCA	1320
Sbjct 1261	GACCTCCCTGCTCTCAGAGCTATTCAACACCTTCAACAGGGTGAAAACGCAGCA	1320
Query 1321	GAAATCTGTGAGTGGATGCCTTCTCCCAAGGTGGATGGGGTAGACCTGTGGTCAGAGCC	1380
Sbjct 1321	GAAATCTGTGAGTGGATGCCTTCTCCCAAGGTGGATGGGGTAGACCTGTGGTCAGAGCC	1380
Query 1381	CCCGGGCAGCACAGCCACTGCCGTCTCCCTGCAGAACCTAGAGCTGCCATCT	1440
Sbjct 1381	CCCGGGCAGCACAGCCACTGCCGTCTCCCTGCAGAACCTAGAGCTGCCATCT	1440
Query 1441	CCCTGCTGCTCATCCAGTCAGGCTGGAGCCCGTGCAGCTCTCAGGAGCTTCCGCA	1500
Sbjct 1441	CCCTGCTGCTCATCCAGTCAGGCTGGAGCCCGTGCAGCTCTCAGGAGCTTCCGCA	1500
Query 1501	ACAGCCTGGTGTATGGCGCCTCGGACAGCAACGCTATGCCACCTGAAGGACCTAGAGG	1560
Sbjct 1501	ACAGCCTGGTGTATGGCGCCTCGGACAGCAACGCTATGCCACCTGAAGGACCTAGAGG	1560

Query	1561	AAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCGGATCCAATCCGGGGCCCCAC	1620
Sbjct	1561	AAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCGGATCCAATCCGGGGCCCCAC	1620
Query	1621	TGGCTTCAGGGACTGGGGAGAGAAACACTGCTGCCCTTTAGCAGTCAGGGCTGA	1680
Sbjct	1621	TGGCTTCAGGGACTGGGGAGAGAAACACTGCTGCCCTTTAGCAGTCAGGGCTGA	1680
Query	1681	CCCAAGAGAACTCACCGTATTCTCATTTCCCTCGTAATCCTCAGGCCTTCTAC	1740
Sbjct	1681	CCCAAGAGAACTCACCGTATTCTCATTTCCCTCGTAATCCTCAGGCCTTCTAC	1740
Query	1741	AACTGGAGGGGAGGGAGGAAATGGATGAATGAGAGAGGGAGGGACAGTGCCCAAGCG	1800
Sbjct	1741	AACTGGAGGGGAGGGAGGAAATGGATGAATGAGAGAGGGAGGGAGGGACAGTGCCCAAGCG	1800
Query	1801	CTTGGCTCTCCTCTTCACTTGCAGAGGCTGGAAGATGGCAGCCCCGGACT	1860
Sbjct	1801	CTTGGCTCTCCTCTTCACTTGCAGAGGCTGGAAGATGGCAGCCCCGGACT	1860
Query	1861	GGGCAGATCTCAATCAGCTCACAGCAAGTTGACACAAAATCGCACACAGTGAACGCA	1920
Sbjct	1861	GGGCAGATCTCAATCAGCTCACAGCAAGTTGACACAAAATCGCACACAGTGAACGCA	1920
Query	1921	CTGCTCAAGAACATACGGGCTCTACTGCTCACAGGAAGGACATGGACAAAGGTCGAGACA	1980
Sbjct	1921	CTGCTCAAGAACATACGGGCTCTACTGCTCACAGGAAGGACATGGACAAAGGTCGAGACA	1980
Query	1981	TTCTGCGCATCGCAGTGCAGTGCAGCTGAGCTGTGGCTCTAGCTGCCGG	2040
Sbjct	1981	TTCTGCGCATCGCAGTGCAGTGCAGCTGAGCTGTGGCTCTAGCTGCCGG	2040
Query	2041	TGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCTGGCTGTGGAAGGTGCTACTCCAGTG	2100
Sbjct	2041	TGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCTGGCTGTGGAAGGTGCTACTCCAGTG	2100
Query	2101	CCCACAGCTTGTCTAAAAAATTAGTTGCACTATTGTTGACTAGGTGCTCTTG	2160
Sbjct	2101	CCCACAGCTTGTCTAAAAAATTAGTTGCACTATTGTTGACTAGGTGCTCTTG	2160
Query	2161	TATAATATTATGGGTGGAGGGGGTGGTATGGAGCAAGGGGCCAGGTTGGGAAGACAAC	2220
Sbjct	2161	TATAATATTATGGGTGGAGGGGGTGGTATGGAGCAAGGGGCCAGGTTGGGAAGACAAC	2220
Query	2221	CTGTAGGGCCTCAGGGTCTATTGGGAAACCGAGCTGGAGTCAGTGGCAGTCTGGCTC	2280
Sbjct	2221	CTGTAGGGCCTCAGGGTCTATTGGGAAACCGAGCTGGAGTCAGTGGCAGTCTGGCTC	2280
Query	2281	GCTGCAATCTCCGCTCTGGGTCAGCGATCTCTGCCAGTCTCCGAATAGTTG	2340
Sbjct	2281	GCTGCAATCTCCGCTCTGGGTCAGCGATCTCTGCCAGTCTCCGAATAGTTG	2340
Query	2341	CGATTCAGGCATGCAAGACCAAGGCTCAGCTAATTTGTATTTGGTAGAGACGGGGT	2400
Sbjct	2341	CGATTCAGGCATGCAAGACCAAGGCTCAGCTAATTTGTATTTGGTAGAGACGGGGT	2400
Query	2401	TTCACCATATTGGCAGTCTGGTCTCCATCTCTGACCTCAGGTAATCCGCCGCTCGG	2460
Sbjct	2401	TTCACCATATTGGCAGTCTGGTCTCCATCTCTGACCTCAGGTAATCCGCCGCTCGG	2460

Query 2461	CCTCCCAAATGCTGGGATTACAGGTATGAGCCACTGGGCCCTCCCTGICCTGTGATT	2520
Sbjct 2461	CCTCCCAAATGCTGGGATTACAGGTATGAGCCACTGGGCCCTCCCTGICCTGTGATT	2520
Query 2521	TAAAAATAATTATACCAAGCAGAAGGACGTCAGACACAGCATGGGCACCTGGCCATGCC	2580
Sbjct 2521	TAAAAATAATTATACCAAGCAGAAGGACGTCAGACACAGCATGGGCACCTGGCCATGCC	2580
Query 2581	AGCCAGTTGGACATTGAGTTGCTGGACTGTCCCTCATGCATTGGTCCACTC	2640
Sbjct 2581	AGCCAGTTGGACATTGAGTTGCTGGACTGTCCCTCATGCATTGGTCCACTC	2640
Query 2641	AGTAGATGCTTGTGAATTC 2660	
Sbjct 2641	AGTAGATGCTTGTGAATTC 2660	
 >dbj DJ052243.1 FLP-mediated Recombination		
Length=2660		
 Score = 4817 bits (2608), Expect = 0.0		
Identities = 2660/2660 (100%), Gaps = 0/2660 (0%)		
Strand=Plus/Plus		
Query 1	GAATTCACTGAATCATGCCAGAACCCCCGCAATCTATTGGCTGTGCTTGGCCCT	60
Sbjct 1	GAATTCACTGAATCATGCCAGAACCCCCGCAATCTATTGGCTGTGCTTGGCCCT	60
Query 61	TTTCCCAACACACACATTCTGCTGGTGGGGAGGGGAAACATGCGGGAGGAGAAAG	120
Sbjct 61	TTTCCCAACACACACATTCTGCTGGTGGGGAGGGGAAACATGCGGGAGGAGAAAG	120
Query 121	GAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGCTCAAGGACTGGCCTATCCTGACA	180
Sbjct 121	GAATAGGATAGAGAGTGGGATGGGTGGTAGGGCTCAAGGACTGGCCTATCCTGACA	180
Query 181	TCTCTCTCCGCGTTCAGTTGGCACCATGGCTGCTGCCAGAGGGCACCCACGTGACCC	240
Sbjct 181	TCTCTCTCCGCGTTCAGTTGGCACCATGGCTGCTGCCAGAGGGCACCCACGTGACCC	240
Query 241	TTAAAGAGAGGACAAGTTGGGGTATCTCTGGCTGACATTCTGTGACAACCCCTACAA	300
Sbjct 241	TTAAAGAGAGGACAAGTTGGGGTATCTCTGGCTGACATTCTGTGACAACCCCTACAA	300
Query 301	CGCTGGTGTGGGGAGGGAAAGATGACAAGTCAGGGGGCATGATCCCAGCATGTGTG	360
Sbjct 301	CGCTGGTGTGGGGAGGGAAAGATGACAAGTCAGGGGGCATGATCCCAGCATGTGTG	360
Query 361	GGAGGAGCTCTAAATTATCATTAGCACAAGCCCGTCAGTGGCCCAGGCCTAAACATG	420
Sbjct 361	GGAGGAGCTCTAAATTATCATTAGCACAAGCCCGTCAGTGGCCCAGGCCTAAACATG	420
Query 421	CAGAGAAAACAGGTGAGGAGAACGCAGCAGAGAGAAGGGCCAGGTATAAAAGGGCCAC	480
Sbjct 421	CAGAGAAAACAGGTGAGGAGAACGCAGCAGAGAGAAGGGCCAGGTATAAAAGGGCCAC	480
Query 481	AAGAGACCAGCTCAAGGATCCAAAGGCCAACTCCCCGAACCACTCAGGGTCCTGTGGAC	540
Sbjct 481	AAGAGACCAGCTCAAGGATCCAAAGGCCAACTCCCCGAACCACTCAGGGTCCTGTGGAC	540

Query	541	AGCTCACTAGCGGAATGGCTGCAAGGTAAGC GCCCTAAATCCCTTGGCACAATGTGT 	600
Sbjct	541	AGCTCACTAGCGGAATGGCTGCAAGGTAAGC GCCCTAAATCCCTTGGCACAATGTGT 	600
Query	601	CTGAGGGGAGAGGCGCGTCTGTAGATGGGACGGGGGACTAACCTCAGGTTGGGG 	660
Sbjct	601	CTGAGGGGAGAGGCGCGTCTGTAGATGGGACGGGGGACTAACCTCAGGTTGGGG 	660
Query	661	CTTAATGAACTTGTAGCTATGCCATCTAACGCCAGTATTGGCCAATCTGAATGTCTCT 	720
Sbjct	661	CTTAATGAACTTGTAGCTATGCCATCTAACGCCAGTATTGGCCAATCTGAATGTCTCT 	720
Query	721	GGTCCCTGGAGGGAGGAG 	780
Sbjct	721	GGTCCCTGGAGGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 	780
Query	781	GAGAGCGCTGGCCTTGTCTCCAGCTCCCTCTGTTGCCCTCGGTTCTCCCCAGGCTC 	840
Sbjct	781	GAGAGCGCTGGCCTTGTCTCCAGCTCCCTCTGTTGCCCTCGGTTCTCCCCAGGCTC 	840
Query	841	CCGGACGTCCCTGCTCTGGCTTTGGCCTGCTGCTCTGGCTTCAAGAGGGCAG 	900
Sbjct	841	CCGGACGTCCCTGCTCTGGCTTTGGCCTGCTGCTCTGGCTTCAAGAGGGCAG 	900
Query	901	TGCCCTCCAACCATTCCCTTATCCAGGCTTTGACAACGCTATGCTCCGCCCGTCG 	960
Sbjct	901	TGCCCTCCAACCATTCCCTTATCCAGGCTTTGACAACGCTATGCTCCGCCCGTCG 	960
Query	961	CTGTACCACTGGCATATGACACCTATCAGGAGTTGTAAGCTTGGTAATGGGTGC 	1020
Sbjct	961	CTGTACCACTGGCATATGACACCTATCAGGAGTTGTAAGCTTGGTAATGGGTGC 	1020
Query	1021	GCTTCAGAGGTGGCAGGAAGGGGTGAATTCCCCCGCTGGGAAGTAATGGGAGGAGACTA 	1080
Sbjct	1021	GCTTCAGAGGTGGCAGGAAGGGGTGAATTCCCCCGCTGGGAAGTAATGGGAGGAGACTA 	1080
Query	1081	AGGAGCTCAGGGTTGTTCTGAAGTAAAAATGCAAGGAGATGAGCATACGCTGAGTGAG 	1140
Sbjct	1081	AGGAGCTCAGGGTTGTTCTGAAGTAAAAATGCAAGGAGATGAGCATACGCTGAGTGAG 	1140
Query	1141	GTTCCCAGAAAAGTAACAATGGGAGCAGGTCTCCAGCATAGACCTTGGTGGCGGTCTT 	1200
Sbjct	1141	GTTCCCAGAAAAGTAACAATGGGAGCAGGTCTCCAGCATAGACCTTGGTGGCGGTCTT 	1200
Query	1201	CTCCCTAGGAAGAACGCTTATCTGAAGGAGCAGAAGTATTCTTCTGCAGAACCCCCA 	1260
Sbjct	1201	CTCCCTAGGAAGAACGCTTATCTGAAGGAGCAGAAGTATTCTTCTGCAGAACCCCCA 	1260
Query	1261	GACCTCCCTGCTCTCAGAGTCTATTCAACACCTTCAACAGGGTAAAACGCAGCA 	1320
Sbjct	1261	GACCTCCCTGCTCTCAGAGTCTATTCAACACCTTCAACAGGGTAAAACGCAGCA 	1320
Query	1321	GAAATCTGTGAGTGGATGCCCTCTCCCAGGTGGATGGGGTAGACCTGTGGTCAGAGCC 	1380
Sbjct	1321	GAAATCTGTGAGTGGATGCCCTCTCCCAGGTGGATGGGGTAGACCTGTGGTCAGAGCC 	1380
Query	1381	CCCGGGCAGCACAGCCACTGCGGTCTCCCTGCAGAACCTAGAGCTGCTCCGCATCT 	1440
Sbjct	1381	CCCGGGCAGCACAGCCACTGCGGTCTCCCTGCAGAACCTAGAGCTGCTCCGCATCT 	1440

Query	1441	CCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTCAGCTCCTCAGGAGCGCTTCGCCA	1500
Sbjct	1441	CCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTCAGCTCCTCAGGAGCGCTTCGCCA	1500
Query	1501	ACAGCCTGGTGTATGGCGCCTCGGACAGCAACGCTATGCCACCTGAAGGACCTAGAGG	1560
Sbjct	1501	ACAGCCTGGTGTATGGCGCCTCGGACAGCAACGCTATGCCACCTGAAGGACCTAGAGG	1560
Query	1561	AAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCAGGATCCAATCCTGGGGCCAC	1620
Sbjct	1561	AAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCAGGATCCAATCCTGGGGCCAC	1620
Query	1621	TGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCCCTTTAGCAGTCAGGCCGCTGA	1680
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Query	1681	CCCAAGAGAACTCACCGTATTCTCATTCCTCGTGAATCCTCAGGCCCTTCTAC	1740
Sbjct	1681	CCCAAGAGAACTCACCGTATTCTCATTCCTCGTGAATCCTCAGGCCCTTCTAC	1740
Query	1741	AACCTGGAGGGAGGGAGGAAAAATGGATGAATGAGAGAGGGAGGGAAACAGTGCCAAAGCG	1800
Sbjct	1741	AACCTGGAGGGAGGGAGGAAAAATGGATGAATGAGAGAGGGAGGGAAACAGTGCCAAAGCG	1800
Query	1801	CTTGGCTCTCCTCTCTTACTTGCAGAGGCTGGAAGATGGCAGCCCCGGACT	1860
Sbjct	1801	CTTGGCTCTCCTCTCTTACTTGCAGAGGCTGGAAGATGGCAGCCCCGGACT	1860
Query	1861	GGGCAGATCTCAATCAGTCTACAGCAAGTTGACACAAAATCGCACACAGTGACGCA	1920
Sbjct	1861	GGGCAGATCTCAATCAGTCTACAGCAAGTTGACACAAAATCGCACACAGTGACGCA	1920
Query	1921	CTGCTCAAGAAACTACGGGCTGCTACTGCTTCAGGAAGGACATGGCAAGGTGAGACA	1980
Sbjct	1921	CTGCTCAAGAAACTACGGGCTGCTACTGCTTCAGGAAGGACATGGCAAGGTGAGACA	1980
Query	1981	TTCCCTGGCATCGTGCAGTGGCCCTCTGGAGGGCAGCTGTGGCTCTAGCTGCCGG	2040
Sbjct	1981	TTCCCTGGCATCGTGCAGTGGCCCTCTGGAGGGCAGCTGTGGCTCTAGCTGCCGG	2040
Query	2041	TGGCATCCCTGTGACCCCTCCCCAGTGCTCTCTGGCTGTTGAAAGGTGCTACTCCAGTG	2100
Sbjct	2041	TGGCATCCCTGTGACCCCTCCCCAGTGCTCTCTGGCTGTTGAAAGGTGCTACTCCAGTG	2100
Query	2101	CCCACCAAGCCTGTCTAAATAAAATTAAAGTGCATCAATTGTTGACTAGGTGCTTGT	2160
Sbjct	2101	CCCACCAAGCCTGTCTAAATAAAATTAAAGTGCATCAATTGTTGACTAGGTGCTTGT	2160
Query	2161	TATAATATTATGGGGTGGAGGGGGGTGGTATGGAGCAAGGGGCAGGTTGGAAAGACAAC	2220
Sbjct	2161	TATAATATTATGGGGTGGAGGGGGTGGTATGGAGCAAGGGGCAGGTTGGAAAGACAAC	2220
Query	2221	CTGTAGGGCCTTCAGGGTCTATCGGAACCAGGCTGGAGTGCAGTGGCAGTCTGGCTC	2280
Sbjct	2221	CTGTAGGGCCTTCAGGGTCTATCGGAACCAGGCTGGAGTGCAGTGGCAGTCTGGCTC	2280
Query	2281	GCTGCAATCTCCGCTCTGGGTCAGCGATTCTCTGCCCTAGTCTCCGAATAGTT	2340
Sbjct	2281	GCTGCAATCTCCGCTCTGGGTCAGCGATTCTCTGCCCTAGTCTCCGAATAGTT	2340

Query	2341	CGATTCAGGCATGCAAGACCAGGCTAGCTAATTTGTATTTTGGTAGAGACGGGGT	2400
Sbjct	2341	CGATTCAGGCATGCAAGACCAGGCTAGCTAATTTGTATTTTGGTAGAGACGGGGT	2400
Query	2401	TTCACCATATTGCCAGTCTGGCTCCATCTCTGACCTCAGGTAATCCGCCGCCCTCGG	2460
Sbjct	2401	TTCACCATATTGCCAGTCTGGCTCCATCTCTGACCTCAGGTAATCCGCCGCCCTCGG	2460
Query	2461	CCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTCCCTGTCCGTGATT	2520
Sbjct	2461	CCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTCCCTGTCCGTGATT	2520
Query	2521	TAAAATAATTATACCAAGCAGAACAGCTTACAGACACAGCATGGGCTACCTGGCCATGCC	2580
Sbjct	2521	TAAAATAATTATACCAAGCAGAACAGCTTACAGACACAGCATGGGCTACCTGGCCATGCC	2580
Query	2581	AGCCAGTTGGACATTGAGTTGCTGGACTGTCTCTCATGCATTGGTCACTC	2640
Sbjct	2581	AGCCAGTTGGACATTGAGTTGCTGGACTGTCTCTCATGCATTGGTCACTC	2640
Query	2641	AGTAGATGCTTGTGAATT	2660
Sbjct	2641	AGTAGATGCTTGTGAATT	2660

>dbj|DD418156.1| AN EXPRESSION CASSETTE AND VECTOR FOR TRANSIENT OR STABLE EXPRESSION OF EXOGENOUS MOLECULES
Length=2660

Score = 4817 bits (2608), Expect = 0.0
Identities = 2660/2660 (100%), Gaps = 0/2660 (0%)
Strand=Plus/Plus

Query	1	GAATTCAAGCACTGAATCATGCCAGAACCCCGCAATCTATTGGCTGTGCTTGGCCCT	60
Sbjct	1	GAATTCAAGCACTGAATCATGCCAGAACCCCGCAATCTATTGGCTGTGCTTGGCCCT	60
Query	61	TTTCCCAACACACACATTCTGTCTGGTGGGGAGGGAAACATGCGGGGAGGAGGAAAG	120
Sbjct	61	TTTCCCAACACACACATTCTGTCTGGTGGGGAGGGAAACATGCGGGGAGGAGGAAAG	120
Query	121	GAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGCTCAAGGACTGGCTATCTGACA	180
Sbjct	121	GAATAGGATAGAGAGTGGGATGGGGTCGGTAGGGGCTCAAGGACTGGCTATCTGACA	180
Query	181	TCTCTCTCCCGTTCAGGTTGGGACCATGGCCTGTCAGGGCACCACGTGACCC	240
Sbjct	181	TCTCTCTCCCGTTCAGGTTGGGACCATGGCCTGTCAGGGCACCACGTGACCC	240
Query	241	TTAAAGAGAGGACAAGTTGGGGTATCTGTGACATTCTGTGACAACCCCTACAA	300
Sbjct	241	TTAAAGAGAGGACAAGTTGGGGTATCTGTGACATTCTGTGACAACCCCTACAA	300
Query	301	CGCTGGTGTGGGGAGGGAAAGATGACAAGTCAGGGGGCATGATCCCAGCATGTG	360
Sbjct	301	CGCTGGTGTGGGGAGGGAAAGATGACAAGTCAGGGGGCATGATCCCAGCATGTG	360
Query	361	GGAGGAGGCTTCAAATTATCCTATTAGCACAAGCCCGTCAGTGGCCCCAGGCTAAACATG	420

Sbjct	361	GGAGGAGCTCTAAATTATCATTAGCACAAGCCGTCAGTGGCCCAGGCCAAACATG	420
Query	421	CAGAGAACAGGTGAGGAGAACCGAGCGAGAGAGAAGGGGCCAGGTATAAAAGGGCCAC	480
Sbjct	421	CAGAGAACAGGTGAGGAGAACCGAGCGAGAGAGAAGGGGCCAGGTATAAAAGGGCCAC	480
Query	481	AAGAGACCAGCTAAGGATCCAAAGGCCAACTCCCGAACCACTCAGGGTCCTGTGGAC	540
Sbjct	481	AAGAGACCAGCTAAGGATCCAAAGGCCAACTCCCGAACCACTCAGGGTCCTGTGGAC	540
Query	541	AGCTCACTAGCGCAATGGCTGCAGGTAGCGCCCTAAATCCCTTGGCACAATGTGT	600
Sbjct	541	AGCTCACTAGCGCAATGGCTGCAGGTAGCGCCCTAAATCCCTTGGCACAATGTGT	600
Query	601	CCTGAGGGAGAGCGCGCTCTGTAGATGGACGGGGCACTAACCTCAGGTTGGGG	660
Sbjct	601	CCTGAGGGAGAGCGCGCTCTGTAGATGGACGGGGCACTAACCTCAGGTTGGGG	660
Query	661	CTTATGAATGTAGCTATGCCATCTAACGCCAGTATTGGCCAATCTGAATGTTCCT	720
Sbjct	661	CTTATGAATGTAGCTATGCCATCTAACGCCAGTATTGGCCAATCTGAATGTTCCT	720
Query	721	GGTCCCCTGGAGGGAGGAG	780
Sbjct	721	GGTCCCCTGGAGGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	780
Query	781	GAGAGCCTGGCCCTTGCTCTCCAGCTCCCTGTGCTCCGGTTCTCCCAAGGCTC	840
Sbjct	781	GAGAGCCTGGCCCTTGCTCTCCAGCTCCCTGTGCTCCGGTTCTCCCAAGGCTC	840
Query	841	CCGGACGTCCCTGCTCTGGCTTTGGCTGCTCTGGCTGTGCTCTGGCTTAAGAGGGCAG	900
Sbjct	841	CCGGACGTCCCTGCTCTGGCTTTGGCTGCTCTGGCTGTGCTCTGGCTTAAGAGGGCAG	900
Query	901	TGCCCCTCCAAACATTCCCTTATCCAGGCTTTGACAACGCTATGCTCCGCCGCTCG	960
Sbjct	901	TGCCCCTCCAAACATTCCCTTATCCAGGCTTTGACAACGCTATGCTCCGCCGCTCG	960
Query	961	CCTGTACCGCTGGCATATGACACCTATCAGGAGTTGTAAGCTTGGTAATGGGTGC	1020
Sbjct	961	CCTGTACCGCTGGCATATGACACCTATCAGGAGTTGTAAGCTTGGTAATGGGTGC	1020
Query	1021	GCTTCAGAGGTGGCAGGAAGGGTGAATTCCCCCGCTGGGAAGTAATGGGAGGAGACTA	1080
Sbjct	1021	GCTTCAGAGGTGGCAGGAAGGGTGAATTCCCCCGCTGGGAAGTAATGGGAGGAGACTA	1080
Query	1081	AGGAGCTCAGGGTGTCTGAAGTGAATAATGCAAGGCAGATGAGCATACGCTGAGTGAG	1140
Sbjct	1081	AGGAGCTCAGGGTGTCTGAAGTGAATAATGCAAGGCAGATGAGCATACGCTGAGTGAG	1140
Query	1141	GTTCCAGAAAAGTAACATGGGAGCAGGTCTCAGCATAGACCTTGGTGGCGCTCTT	1200
Sbjct	1141	GTTCCAGAAAAGTAACATGGGAGCAGGTCTCAGCATAGACCTTGGTGGCGCTCTT	1200
Query	1201	CTCCTAGGAAGAAGCCATATCCTGAAGGAGCAGAACAGTATTCTCTGCAGAACCCCCA	1260
Sbjct	1201	CTCCTAGGAAGAAGCCATATCCTGAAGGAGCAGAACAGTATTCTCTGCAGAACCCCCA	1260
Query	1261	GACCTCCCTGCTCTCAGAGTCTATTCAACACCTTCAACAGGGTGAACAGCAGCA	1320

Sbjct	1261	GACCTCCCTCTGTTCTAGAGCTATTCAAACACCTTCAAACAGGGTGAAACGCAGCA	1320
Query	1321	GAAATCTGTGAGTGGATGCCCTCTCCCAAGGTGGATGGGGTAGACCTGTGGTCAGAGCC	1380
Sbjct	1321	GAAATCTGTGAGTGGATGCCCTCTCCCAAGGTGGATGGGGTAGACCTGTGGTCAGAGCC	1380
Query	1381	CCCGGGCAGCACAGCCACTGCCGCTCTCCCTGCAAGAACCTAGAGCTGCTCCGCATCT	1440
Sbjct	1381	CCCGGGCAGCACAGCCACTGCCGCTCTCCCTGCAAGAACCTAGAGCTGCTCCGCATCT	1440
Query	1441	CCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGCAGCTCCTCAGGAGCGTCTTCGCCA	1500
Sbjct	1441	CCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGCAGCTCCTCAGGAGCGTCTTCGCCA	1500
Query	1501	ACAGCTGGTGTATGGCCCTCGGACAGCAACGCTATGCCACCTGAAGGACCTAGAGG	1560
Sbjct	1501	ACAGCTGGTGTATGGCCCTCGGACAGCAACGCTATGCCACCTGAAGGACCTAGAGG	1560
Query	1561	AAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCAAGGATCAAATCCTGGGGCCCCAC	1620
Sbjct	1561	AAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCAAGGATCAAATCCTGGGGCCCCAC	1620
Query	1621	TGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCCCTTTTAGCAGTCAGGCCTGTA	1680
Sbjct	1621	TGGCTTCCAGGGACTGGGGAGAGAAACACTGCTGCCCTTTTAGCAGTCAGGCCTGTA	1680
Query	1681	CCCAAGAGAACTCACCGTATTCTCATTCCCTCGTAATCCTCAGGCCTTCTAC	1740
Sbjct	1681	CCCAAGAGAACTCACCGTATTCTCATTCCCTCGTAATCCTCAGGCCTTCTAC	1740
Query	1741	AACCTGGAGGGAGGGAGGAAATGGATGAATGAGAGAGGGAGGGAAACAGTGCCCAAGCG	1800
Sbjct	1741	AACCTGGAGGGAGGGAGGAAATGGATGAATGAGAGAGGGAGGGAAACAGTGCCCAAGCG	1800
Query	1801	CTTGGCTCTCCTTCTTCTTCACTTGTGAGAGGCTGGAAGATGGCAGCCCCGGACT	1860
Sbjct	1801	CTTGGCTCTCCTTCTTCTTCACTTGTGAGAGGCTGGAAGATGGCAGCCCCGGACT	1860
Query	1861	GGGCAGATCTCAATCAGTCTACAGCAAGTTGACACAAATCGCACACGATGACGCA	1920
Sbjct	1861	GGGCAGATCTCAATCAGTCTACAGCAAGTTGACACAAATCGCACACGATGACGCA	1920
Query	1921	CTGCTCAAGAAACTACGGGCTGCTACTGCTTCAGGAAGGACATGGCAAGGTGAGACA	1980
Sbjct	1921	CTGCTCAAGAAACTACGGGCTGCTACTGCTTCAGGAAGGACATGGCAAGGTGAGACA	1980
Query	1981	TTCTCGCATCGTGCAGTGGCGCTCTGGAGGGCAGCTGTGGCTTCTAGCTGCCCGG	2040
Sbjct	1981	TTCTCGCATCGTGCAGTGGCGCTCTGGAGGGCAGCTGTGGCTTCTAGCTGCCCGG	2040
Query	2041	TGGCATCCCTGTGACCCCTCCCCAGTGCTCTCTGGCTGTGGAGGTGCTACTCCAGTG	2100
Sbjct	2041	TGGCATCCCTGTGACCCCTCCCCAGTGCTCTCTGGCTGTGGAGGTGCTACTCCAGTG	2100
Query	2101	CCCACAGCTTGTCTAAATAAAATTAGTGCATATTGTTGACTAGGTGCTTGTG	2160
Sbjct	2101	CCCACAGCTTGTCTAAATAAAATTAGTGCATATTGTTGACTAGGTGCTTGTG	2160
Query	2161	TATAATATTATGGGGTGGAGGGGGTGTATGGAGCAAGGGGCCAGGTGGAAAGACAAC	2220

Sbjct	2161	TATAATATTATGGGTGGAGGCAGGGTGGTATGGAGCAAGGGGCAGGTTGGGAAGACAAC	2220
Query	2221	CTGTAAGGGCCTCAGGGTCTATTGGGAACCAGGCTGGAGTGCAGTGGCAGTCTGGCTC	2280
Sbjct	2221	CTGTAAGGGCCTCAGGGTCTATTGGGAACCAGGCTGGAGTGCAGTGGCAGTCTGGCTC	2280
Query	2281	GCTGCAATCTCCGCTCTGGGTTCAAGCGATTCTCCTGCCTCAGTCTCCGAATAGTTG	2340
Sbjct	2281	GCTGCAATCTCCGCTCTGGGTTCAAGCGATTCTCCTGCCTCAGTCTCCGAATAGTTG	2340
Query	2341	CGATTCCAGGCATGCAAGACCAAGGCTCAGCTAATTTGTATTTGGTAGAGACGGGT	2400
Sbjct	2341	CGATTCCAGGCATGCAAGACCAAGGCTCAGCTAATTTGTATTTGGTAGAGACGGGT	2400
Query	2401	TTCACCATATTGCCAGTCTGGTCTCCATCTCTGACCTCAGGTAAATCCGCCCGCTGG	2460
Sbjct	2401	TTCACCATATTGCCAGTCTGGTCTCCATCTCTGACCTCAGGTAAATCCGCCCGCTGG	2460
Query	2461	CCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTCCCTGTCTGTGATT	2520
Sbjct	2461	CCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTCCCTGTCTGTGATT	2520
Query	2521	TAAAATAATTATACACAGCAGAAGGACGTCCAGACACAGCATGGGCTACCTGGCCATGCC	2580
Sbjct	2521	TAAAATAATTATACACAGCAGAAGGACGTCCAGACACAGCATGGGCTACCTGGCCATGCC	2580
Query	2581	AGCCAGTTGGACATTGAGTTGTTGCTGGACTGTCTCTCATGATTGGTCACTC	2640
Sbjct	2581	AGCCAGTTGGACATTGAGTTGTTGCTGGACTGTCTCTCATGATTGGTCACTC	2640
Query	2641	AGTAGATGCTTGTGAATTC	2660
Sbjct	2641	AGTAGATGCTTGTGAATTC	2660

>obj|E00140.1| Genomic DNA encoding human growth hormone
Length=2660

Score = 4795 bits (2596), Expect = 0.0
Identities = 2656/2660 (99%), Gaps = 0/2660 (0%)
Strand=Plus/Plus

Query	1	GAATTCACTGAAATCATGCCAGAACCCCCGCAATCTATTGGCTGTGCTTGGCCCT	60
Sbjct	1	GAATTCACTGAAATCATGCCAGAACCCCCGCAATCTATTGGCTGTGCTTGGCCCT	60
Query	61	TTTCCCAAACACACACATTCTGTCTGGTGGGTGAGGGRAACATGCGGGGAGGAGRAAG	120
Sbjct	61	TTTCCCAAACACACACATTCTGTCTGGTGGGTGAGGGAAACATGCGGGGAGGAGGAAG	120
Query	121	GAATAGGATAGAGAGTGGGATGGGTGGTCAAGGACTGGCTATCTGACA	180
Sbjct	121	GAATAGGATAGAGAGTGGGATGGGTGGTCAAGGACTGGCTATCTGACA	180
Query	181	TCTCTCCCGCTCAGGTTGGGCCACCATGGCCTGTCGCGAGGGCACCCACGTGACCC	240
Sbjct	181	TCTCTCCCGCTCAGGTTGGGCCACCATGGCCTGTCGCGAGGGCACCCACGTGACCC	240
Query	241	TTAAAGAGGAGACAAGTGGGGTGTATCTGGCTGACATTCTGTGACAACCCCTACAA	300

Sbjct	1141	GTTCAGAGAAAGTAAACATGGGAGCAGGTCTCCAGCATAGACCTGGTGGCGGTCTT	1200
Query	1201	CTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAGATTCTGCAGAACCCCCA	1260
Sbjct	1201	CTCCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAGATTCTGCAGAACCCCCA	1260
Query	1261	GACCTCCCTGCTCTCAGAGTCTATTCAACACCTTCAACAGGGTAAAACGCAGCA	1320
Sbjct	1261	GACCTCCCTGCTCTCAGAGTCTATTCAACACCTTCAACAGGGTAAAACGCAGCA	1320
Query	1321	GAAATCTGTGAGTGGATGCCTCTCCCAGGTGGATGGGTAGACCTGTGGTCAGAGCC	1380
Sbjct	1321	GAAATCTGTGAGTGGATGCCTCTCCCAGGTGGATGGGTAGACCTGTGGTCAGAGCC	1380
Query	1381	CCCGGGCAGCACGCCACTGCCGTCTCCCTGCAGAACCTAGAGCTCGCCATCT	1440
Sbjct	1381	CCCGGGCAGCACGCCACTGCCGTCTCCCTGCAGAACCTAGAGCTCGCCATCT	1440
Query	1441	CCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGCAGCTCCAGGAGCTTCCGCA	1500
Sbjct	1441	CCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGCAGCTCCAGGAGCTTCCGCA	1500
Query	1501	ACAGCCTGGTGTATGGCGCCTCGGACAGCAACGCTATGCCACCTGAAGGACCTAGAGG	1560
Sbjct	1501	ACAGCCTGGTGTATGGCGCCTCGGACAGCAACGCTATGCCACCTGAAGGACCTAGAGG	1560
Query	1561	AAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCAGGATCCAATCTGGGGCCCCAC	1620
Sbjct	1561	AAGGCATCCAAACGCTGATGTGGGTGAGGGTGGCACCAGGATCCAATCTGGGGCCCCAC	1620
Query	1621	TGGCTTCAGGGACTGGGGAGAGAAACACTGCTGCCCTTTTAGCAGTCAGGCCGTGA	1680
Sbjct	1621	TGGCTTCAGGGACTGGGGAGAGAAACACTGCTGCCCTTTTAGCAGTCAGGCCGTGA	1680
Query	1681	CCCAAGAGAACCTACCGTATTCTCATTCCTCGTGAATCTCCAGGCCCTTCTAC	1740
Sbjct	1681	CCCAAGAGAACCTACCGTATTCTCATTCCTCGTGAATCTCCAGGCCCTTCTAC	1740
Query	1741	AACCTGGAGGGAGGGAGGAAATGGATGAATGAGAGAGGGAGGGAACAGTGCCAACCG	1800
Sbjct	1741	AACCTGGAGGGAGGGAGGAAATGGATGAATGAGAGAGGGAGGGAACAGTGCCAACCG	1800
Query	1801	CTTGGCCTCTCTCTTCTTCACTTGCAGAGGCTGGAAAGATGGCAGCCCCCGGACT	1860
Sbjct	1801	CTTGGCCTCTCTCTTCTTCACTTGCAGAGGCTGGAAAGATGGCAGCCCCCGGACT	1860
Query	1861	GGGCAGATCTCAATCAGTCTACAGCAAGTTGACACAAAATCGCACACGATGACGA	1920
Sbjct	1861	GGGCAGATCTCAATCAGTCTACAGCAAGTTGACACAAAATCGCACACGATGACGA	1920
Query	1921	CTGCTCAAGAACATACGGGCTGCTACTGCTCAGGAAGGACATGGACAAGGTCGAGACA	1980
Sbjct	1921	CTGCTCAAGAACATACGGGCTGCTACTGCTCAGGAAGGACATGGACAAGGTCGAGACA	1980
Query	1981	TTCCCTGCGCATCGTGCAGTGCCTCTGGAGGGCAGCTGTGGCTTCTAGCTGCCCGG	2040
Sbjct	1981	TTCCCTGCGCATCGTGCAGTGCCTCTGGAGGGCAGCTGTGGCTTCTAGCTGCCCGG	2040
Query	2041	TGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCCTGGCTGTGGAGGTGACTCCAGTG	2100

Sbjct	2041	TGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCCTGGCTGTGGAAGGTGCTACTCCAGTG	2100
Query	2101	CCCACCAGCCTGTCTAATAAAATTAAAGTGCATCATTTGTTGACTAGGTGTCCTTG	2160
Sbjct	2101	CCCACCAGCCTGTCTAATAAAATTAAAGTGCATCATTTGTTGACTAGGTGTCCTTG	2160
Query	2161	TATAATATTATGGGGTGGAGGGGGTGGTATGGAGCAAGGGGCCAGGTTGGAAAGACAAC	2220
Sbjct	2161	TATAATATTATGGGGTGGAGGGGGTGGTATGGAGCAAGGGGCCAGGTTGGAAAGACAAC	2220
Query	2221	CTGTAGGGCCTCAGGGTCTATCGGGAACCGAGGCTGGAGTGCAGTGGCAGTCTGGCTC	2280
Sbjct	2221	CTGTAGGGCCTCAGGGTCTATCGGGAACCGAGGCTGGAGTGCAGTGGCAGTCTGGCTC	2280
Query	2281	GCTGCAATCTCCGCCTCTGGGTCAAACCGATTCTCCGCCTCAGTCTCCGAATAGTTG	2340
Sbjct	2281	GCTGCAATCTCCGCCTCTGGGTCAAACCGATTCTCCGCCTCAGTCTCCGAATAGTTG	2340
Query	2341	CGATTCCAGGCATGCAAGACCAAGGCTCAGCTAATTTGTATTTGGTAGAGACGGGGT	2400
Sbjct	2341	GGATTCCAGGCATGCAAGACCAAGGCTCAGCTAATTTGTATTTGGTAGAGACGGGGT	2400
Query	2401	TTCACCATATTGGCAGTCTGGTCTCATCTCTGACCTCAGGTAATCCGCCCGCTCGG	2460
Sbjct	2401	TTCACCATATTGGCAGTCTGGTCTCATCTCTGACCTCAGGTAATCCGCCCGCTCGG	2460
Query	2461	CCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTCCCTGTCTGTGATT	2520
Sbjct	2461	CCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTCCCTGTCTGTGATT	2520
Query	2521	TAAAATAATTATACCAAGCAGAACAGGACGTCCAGACACAGCATGGGTACCTGGCATGCC	2580
Sbjct	2521	TAAAATAATTATACCAAGCAGAACAGGACGTCCAGACACAGCATGGGTACCTGGCATGCC	2580
Query	2581	AGCCAGTTGGACATTGAGTTGGCTTGGCACTGTCTCTCATGCATTGGTCACTC	2640
Sbjct	2581	AGCCAGTTGGACATTGAGTTGGCTTGGCACTGTCTCTCATGCATTGGTCACTC	2640
Query	2641	AGTAGATGCTTGTGAATTC	2660
Sbjct	2641	AGTAGATGCTTGTGAATTC	2660

>emb|AX719120.1| Sequence 1 from Patent EP1295938
Length=5002

Score = 4724 bits (2558), Expect = 0.0
Identities = 2651/2668 (99%), Gaps = 13/2668 (0%)
Strand=Plus/Plus

Query	1	GAATTCACTGAATCATGCCAGAACCCCGCAATCTATGGCTGTGCTTGGCCCT	60
Sbjct	1589	GAATTCACTGAATCATGCCAGAACCCCGCAATCTATGGCTGTGCTTGGCCCT	1648
Query	61	TTTCCCAACACACACATTCTGCTGGTGGGGAGGGAAACATGCGGGGAGGAGGAAAG	120
Sbjct	1649	TTTCCCAACACACACATTCTGCTGGTGGGGAGGGAAACATGCGGGGAGGAGGAAAG	1708
Query	121	GAATAGGATAGAGAGTGGGATGGGTGCGTAGGGTCTCAAGGACTGGCTATCCTGACA	180

Sbjct	1709	GAATAGGATAGAGAGTGGGATGGGTCGGTAGGGGCTCAAGGACTGG-CTATCCTGACA	1767
Query	181	TCTCTTCGGCGTTCAGGGGACCATGGCCTGCTGCCAGAGGGCACCCACGTGACCC	240
Sbjct	1768	TCTCTTCGGCGTTCAGGGGACCATGGCCTGCTGCCAGAGGGCACCCACGTGACCC	1827
Query	241	TTAAAGAGAGGACAAGTGGGGTATCTCTGGCTGACATTCTGTGACAACCTCACAA	300
Sbjct	1828	TTAAAGAGAGGACAAGTGGGTGATCTCT-GCTGACATTCTGTGACAACCTCACAA	1886
Query	301	CGCTGGTGTGGGGAGGGAAAGATGACAAGTCAGGGGGCATGATCCCAGCATGTGTG	360
Sbjct	1887	CGCTGGTGTGGGGAGGGAAAGATGACAAGTCAGGGGGCATGATCCCAGCATGTGTG	1946
Query	361	GGAGGAGCTCTAAATTATCCTAGCACAAGCCGTCACTGGCCCAGGCCCTAACATG	420
Sbjct	1947	GGAGGAGCTCTAAATTATCCTAGCACAAGCCGTCACTGGCCCAGGCCCTAACATG	2006
Query	421	CAGAGAACAGGTGAGGAGAACGAGCGAGAGAGAACGGGCCAGGTATAAAAGGGCCAC	480
Sbjct	2007	CAGAGAACAGGTGAGGAGAACGAGCGAGAGAACGGGCCAGGTATAAAAGGGCCAC	2066
Query	481	AAGAGACCAGCTAAGGATCCAAAGGCCAACTCCCCAACCTCAGGGTCTGTGGAC	540
Sbjct	2067	AAGAGACCAGCTAAGGATCCAAAGGCCAACTCCCCAACCTCAGGGTCTGTGGAC	2126
Query	541	AGCTCA-CTAGCGGCAATGGCTGAGGTAAAGGCCCTAAATCCCTT-GGCACATGT	598
Sbjct	2127	AGCTCACCTAGCGGCAATGGCTGAGGTAAAGGCCCTAAATCCCTTGGGCACATGT	2186
Query	599	GTCCTGAGGGGAGAGGCCGCTCTGTAGATGGGACGGGGCACTAACCTCAGGTTGG	658
Sbjct	2187	GTCCTGAGGGGAGAGGCCGCTCTGTAGATGGGACGGGGCACTAACCTCAGGTTGG	2246
Query	659	GGCTTATGAATGTTAGTATCGCCATCTAACGCCAGTATTGGCCAATCTGAATGTC	718
Sbjct	2247	GGCTTATGAATGTTAG-TATGCCCATCTAACGCCAGTATTGGCCAATCTGAATGTC	2305
Query	719	CTGGTCCCTGGA-GGAGGCAgagagagagagagagaaaaaaaACCAGCTCTGGAAC	777
Sbjct	2306	CTGGTCCCTGGAGGGAGGCAGAGAGAGAGAGAGAGAGAGAGAGAGACCAGCTCTGGAAC	2365
Query	778	AGGGAGAGCGCTGGCCTTGTCTCCAGCTCCCTCTGTGCTCCGGTTCTCCCCAGG	837
Sbjct	2366	AGGGAGAGCGCTGGCCTTGTCTCCAGCTCCCTGTGCTCCGGTTCTCCCCAGG	2425
Query	838	CTCCCGGACGTCCTGTCCTGGCTTGGCTCTGGCTCTGGCTCAAGAGGG	897
Sbjct	2426	CTCCCGGACGTCCTGTCCTGGCTTGGCTCTGGCTCAAGAGGG	2485
Query	898	CAGTGCCTCCCAACCATTCCCTATCCAGGTTTGACAACGCTATGCTCCGCCCG	957
Sbjct	2486	CAGTGCCTCCCAACCATTCCCTATCCAGGTTTGACAACGCTATGCTCCGCCCG	2545
Query	958	TGCCCTGTACCGAGCTGGCATATGACACCTATCAGGAGTTGTAAGCTTGGGTAATGGG	1017
Sbjct	2546	TGCCCTGTACCGAGCTGGCATATGACACCTATCAGGAGTTGTAAGCTTGGGTAATGGG	2605
Query	1018	TGCGCTTCAGGGTGGCAGGAAGGGTGAATTCCCCGCTGGGAAGTAATGGGAGGAGA	1077

Sbjct	2606	TGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTCCCCCGCTGGGAAGTAATGGGAGGAGA	2665
Query	1078	CTAAGGAGCTCAGGGTTGTTTCTGAAGTGAAAATGCAGGCAGATGAGCATACGCTGAGT	1137
Sbjct	2666	CTAAGGAGCTCAGGGTTGTTTCTGAAGTGAAAATGCAGGCAGATGAGCATACGCTGAGT	2725
Query	1138	GAGGTCCCAGAAAAGTAACAATGGGAGCAGGGTCCACAGCATAGACCTGGTGGCGGTC	1197
Sbjct	2726	GAGGTCCCAGAAAAGTAACAATGGGAGCAGGGTCTCCACAGCATAGACCTGGTGGCGGTC	2785
Query	1198	CTTCTCTAGGAAGAACCTATACCTGAAGGAGCAGAAGTATTCTTCAGAACACCCC	1257
Sbjct	2786	CTTCTCTAGGAAGAACCTATACCTGAAGGAGCAGAAGTATTCTTCAGAACACCCC	2845
Query	1258	CCAGACCTCCCTGCTCTCAGAGTCTATTCAACACCTTCAACAGGGTGAAACGCA	1317
Sbjct	2846	CCAGACCTCCCTGCTCTCAGAGTCTATTCAACACCTTCAACAGGGTGAAACGCA	2905
Query	1318	GCAGAAATCTGTGAGTGGATGCCTTCTCCCAGGTGGGATGGGTAGACCTGTGGTCAGA	1377
Sbjct	2906	GCAGAAATCTGTGAGTGGATGCCTTCTCCCAGGTGGGATGGGTAGACCTGTGGTCAGA	2965
Query	1378	GCCCCCGGGCAGCACAGCCACTGCCCTCTCAGAACACTAGAGCTGCTCCCGCA	1437
Sbjct	2966	GCCCCCGGGCAGCACAGCCACTGCCCTCTCAGAACACTAGAGCTGCTCCCGCA	3025
Query	1438	TCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGAGCTCTCAGGAGCTTCTCG	1497
Sbjct	3026	TCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGAGCTCTCAGGAGCTTCTCG	3085
Query	1498	CCAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGTCTATGCCACCTGAAGGACCTAG	1557
Sbjct	3086	CCAACAGCCTGGTGTATGGCGCCTCGGACAGCAACGTCTATGCCACCTGAAGGACCTAG	3145
Query	1558	AGGAAGGCATCCAACGCTGATGTGGGTGAGGGTGGCACCAGG-ATCC--AATCTGGGG	1614
Sbjct	3146	AGGAAGGCATCCAACGCTGATGTGGGTGAGGGTGGCACCAGGGATCCCCAATCTGGGG	3205
Query	1615	CCCCACTGGCTCCAGGGACTGGGAGAGAAACACTGCTGCCCTTTTAGCAGTCAGG	1674
Sbjct	3206	CCCCACTGGCTCCAGGGACTGGGAGAGAAACACTGCTGCCCTTTTAGCAGTCAGG	3265
Query	1675	CGCTGACCCAAGAGAAACTCACCGTATTCTCATTTCCCTCGTGAATCCTCCAGGGCTTT	1734
Sbjct	3266	CGCTGACCCAAGAGAAACTCACCGTATTCTCATTTCCCTCGTGAATCCTCCAGGGCTTT	3325
Query	1735	CTCTACAACCTGGAGGGGAGGGAGGAAATGGATGAATGAGAGAGGGAGGGAAACAGTGC	1794
Sbjct	3326	CTCTACAACCTGGAGGGGAGGGAGGAAATGGATGAATGAGAGAGGGAGGGAAACAGTGC	3385
Query	1795	CAAGCGCTTGGCCTCTCTCTCAGTGCAGAGGCTGGAAGATGGCAGCCCC	1854
Sbjct	3386	CAAGCGCTTGGCCTCTCTCTCAGTGCAGAGGCTGGAAGATGGCAGCCCC	3445
Query	1855	CGGACTGGCAGATCTTCAATCAGCTTACAGCAAGTTGACACAAAATGCACAACGAT	1914
Sbjct	3446	CGGACTGGCAGATCTTCAATCAGCTTACAGCAAGTTGACACAAAATGCACAACGAT	3505
Query	1915	GACGCAGTCTCAAGAAACTACGGGCTGCTACTGCTCAGGAAGGACATGGACAAGGTC	1974

Sbjct	3506	GAGCAGCTGCTCAAGAACACTAGGGCTGCTACTGCTTCAGGAAGGACATGGCACAGGTC	3565
Query	1975	GAGACATTCTCGCGCATCGCAGTGCAGTCAGCTGGAGGGCAGCTGTGGCTTCTAGCTG	2034
Sbjct	3566	GAGACATTCTCGCGCATCGCAGTGCAGTCAGCTGGAGGGCAGCTGTGGCTTCTAGCTG	3625
Query	2035	CCGGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCCTCCTGGCTGTGGAAGGTGCTACT	2094
Sbjct	3626	CCGGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCCTCCTGGCTGTGGAAGGTGCTACT	3685
Query	2095	CCAGTGCCCCACAGCCTTGTCTTAATAAAATAAGTGCATATTGTTGACTAGGTG	2154
Sbjct	3686	CCAGTGCCCCACAGCCTTGTCTTAATAAAATAAGTGCATATTGTTGACTAGGTG	3745
Query	2155	TCCTTGATAATATTATGGGGTGGAGGCGGGTGGTATGGAGCAAGGGCCAGGGTGGAA	2214
Sbjct	3746	TCCTTGATAATATTATGGGGTGGAGGCGGGTGGTATGGAGCAAGGGC-AGGGTGGAA	3804
Query	2215	GACAACCTGTAGGGCCTTCAGGGTCTATTCCGGAACCCAGGCTGGAGTCAGTGGCA-G-T	2272
Sbjct	3805	GACAACCTGTAGGGCCTTCAGGGTCTATT-GGGAACCCAGGCTGGAGTCAGTGGCACGAT	3863
Query	2273	CTTGGCTCGCTCGAACATCCGCCCTCCGGGTTCAAGCGATTCTCTGCCTCAGTCCCCG	2332
Sbjct	3864	CTTGGCTCGCTCGAACATCCGCCCTCCGGGTTCAAGCGATTCTCTGCCTCAGTCCCCG	3923
Query	2333	AATAGTTGCAGTCCAGGCATGCAAGGACAGGCTCAGCTAATTTGTATTTGGTAGA	2392
Sbjct	3924	AATAGTTGGGATTCAGGCATGCAAGGACAGGCTCAGCTAATTTGTATTTGGTAGA	3983
Query	2393	GACGGGGTTTCACCATATTGGCCAGTCTGGTCTCCATCTCTGACCTCAGGTAATCCGCC	2452
Sbjct	3984	GACGGGGTTTCACCATATTGGCCAGTCTGGTCTCCATCTCTGACCTCAGGTAATCCGCC	4043
Query	2453	CGCCTCGGCCCTCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTCCCTGTCC	2512
Sbjct	4044	CGCCTCGGCCCTCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTCCCTGTCC	4103
Query	2513	TGTGATTTAAAAATAATTACCAAGCAGAACAGGACGTCCAGACACAGCATGGCTACCTGG	2572
Sbjct	4104	TGTGATTTAAAAATAATTACCAAGCAGAACAGGACGTCCAGACACAGCATGGCTACCTGG	4163
Query	2573	CCATGCCAGCCAGTGGACATTGAGTTGCTTGGCACTGTCCCTCATGCAATTGG	2632
Sbjct	4164	CCATGCCAGCCAGTGGACATTGAGTTGCTTGGCACTGTCCCTCATGCAATTGG	4223
Query	2633	GTCCACTCAGTAGATGCTTGTGAATTIC 2660	
Sbjct	4224	GTCCACTCAGTAGATGCTTGTGAATTIC 4251	

Score = 204 bits (110), Expect = 4e-49
Identities = 213/261 (81%), Gaps = 14/261 (5%)
Strand=Plus/Plus

Query	2250	CCAGGCTGGAGTCAGT-G-GCAGTCTGGCTCGCTGCAATCTCCGCTCTGGGTTCAA	2307
Sbjct	646	CCAGGCTGGAGTCAGTGGCCAATCTGGCTCACAGCAACCTCTGCCCTCTGGGTTCAA	705
Query	2308	GCGATTCTCTGCCTCAGTCCGAA-TAGTTGCGATTCCAGGCA-TGCAAGACCAAGG	2364

Subjct 706		762
Query 2365	-CTCAGCTAATTTGTATTTT-GGTAGAGACGGGTTTCACCATATTGCCAGTCTGG	2422
Subjct 763	AC-CAGCTAATTTGTATTTAGG-AGAGATGGAGTTGCCATGTGGTTAGCCTGG	820
Query 2423	TCCTC-CATCTCTGACCTCAGTAAATCGCCGCCCTCGGCCCTCCAAATGCTGGGATTA	2481
Subjct 821	TCTTGCA-CTCCCTGACCTTAAGTGATCCACCCACCTCAGCCTCCAAAGTGTGGGATTA	879
Query 2482	CAGGTATGAGCCACTGGGCC 2502	
Subjct 880	TAGGCATGAGCCACCGTGCCC 900	

>emb|AX659146.1| Sequence 1 from Patent WO02101002
Length=5002

Score = 4724 bits (2558), Expect = 0.0
Identities = 2651/2668 (99%), Gaps = 13/2668 (0%)
Strand=Plus/Plus

Query 1	GAATT CAG CACT GAA T CAT GCC CAG A A C C C C G C A A T C T A T T G G C T G T G C T T T G G C C C T	60
Subjct 1589	GAATT CAG CACT GAA T CAT GCC CAG A A C C C C G C A A T C T A T T G G C T G T G C T T T G G C C C T	1648
Query 61	TTT C C C A A C A C A C A C A T T C T G T C T G G T G G G A G G G A A A C A T G C G G G G A G G G A A A G	120
Subjct 1649	TTT C C C A A C A C A C A C A T T C T G T C T G G T G G G T G G A G G G A A A C A T G C G G G G A G G G A A A G	1708
Query 121	GAATAGGATAGAGATGGATGGGTGCGTAGGGTCTCAAGGACTGGCTATCTGACA	180
Subjct 1709	GAATAGGATAGAGATGGATGGGTGCGTAGGGTCTCAAGGACTGG-CTATCTGACA	1767
Query 181	T C C T T C T C C G C G T T C A G G T T G G C C A C C A T G G C C T G C T G C C A G A G G G C A C C C A C T G G A C C	240
Subjct 1768	T C C T T C T C C G C G T T C A G G T T G G C C A C C A T G G C C T G C T G C C A G A G G G C A C C C A C T G G A C C	1827
Query 241	T T T A A A G A G A G G A C A A G T T G G G T G G T A T C T G G C T G A C A T T C T G T G C A C A A C C C T C A C A A	300
Subjct 1828	T T T A A A G A G A G G A C A A G T T G G G T G G T A T C T C T - G C T G A C A T T C T G T G C A C A A C C C T C A C A A	1886
Query 301	C G C T G G T G A T G G T G G G A A G G G A A A G A T G A C A A G T C A G G G G C A T G A T C C C A G C A T G T G	360
Subjct 1887	C G C T G G T G A T G G T G G G A A G G G A A A G A T G A C A A G T C A G G G G C A T G A T C C C A G C A T G T G	1946
Query 361	G G A G G A G C T T C T A A A T T A T C C A T T A G C A C A A G C C G T C A G T G G C C C A G G C T A A A C A T G	420
Subjct 1947	G G A G G A G C T T C T A A A T T A T C C A T T A G C A C A A G C C G T C A G T G G C C C A G G C T A A A C A T G	2006
Query 421	C A G A G A A A C A G G T G A G G G A A G C A G C G A G A G G A G A A G G G G C C A G G T A T A A A A A G G G G C C A C	480
Subjct 2007	C A G A G A A A C A G G T G A G G G A A G C A G C G A G A G G A G A A G G G G C C A G G T A T A A A A A G G G G C C A C	2066
Query 481	A A G A G A C C G C T C A A G G A T C C A A G G C C A A C T C C C G A A C C A C T C A G G G T C C T G T G G A C	540
Subjct 2067	A A G A G A C C G C T C A A G G A T C C A A G G C C A A C T C C C G A A C C A C T C A G G G T C C T G T G G A C	2126
Query 541	A G C T C A - C T A G C G G C A A T G G C T G C A G G T A A G C G C C C T A A A T C C C T T - G G C A C A T G T	598

Sbjct	2127	AGCTCACCTAGCGGCAATGGCTGCAGGTAAAGCGCCCTAAACCTTGGGCACAAATGT	2186
Query	599	GTCTTGAGGGGAGAGGCGGCCTCTGTAGATGGGACGGGGCACTAACCTCAGGTTGG	658
Sbjct	2187	GTCTTGAGGGGAGAGGCGGCCTCTGTAGATGGGACGGGGCACTAACCTCAGGTTGG	2246
Query	659	GGCTTATGAATGTTAGCTATGCCCATCTAACGCCAGTATTGCCAATCTCTGAATGTT	718
Sbjct	2247	GGCTTATGAATGTTAG-TATGCCCATCTAACGCCAGTATTGCCAATCTCTGAATGTT	2305
Query	719	CTGGTCCCTGGA-GGAGGCagagagagagagagaaaaaaaACCAAGCTCTGGAAC	777
Sbjct	2306	CTGGTCCCTGGAGGGAGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAC	2365
Query	778	AGGGAGAGCGCTGGCCTTGTCTCCAGCTCCCTCTGTGCCTCCGGTTCTCCCCAGG	837
Sbjct	2366	AGGGAGAGCGCTGGCCTTGTCTCCAGCTCCCTCTGTGCCTCCGGTTCTCCCCAGG	2425
Query	838	CTCCCGGACGCTCCCTGCTCCCTGGCTTTGGCTCTGCTCTGGCTCTGGCTCAAGAGGG	897
Sbjct	2426	CTCCCGGACGCTCCCTGCTCCCTGGCTTTGGCTCTGACTGCTCTGGCTCAAGAGGG	2485
Query	898	CAGTGCCTCCAAACCATCCCTTATCCAGGTTTGACAACGCTATGCTCCGCCCG	957
Sbjct	2486	CAGTGCCTCCAAACCATCCCTTATCCAGGTTTGACAACGCTATGCTCCGCCCG	2545
Query	958	TCGCCTGTACCAAGCTGGCATATGACACCTATCAGGAGTTGTAAGCTTGGGTAATGGG	1017
Sbjct	2546	TCGCCTGTACCAAGCTGGCATATGACACCTATCAGGAGTTGTAAGCTTGGGTAATGGG	2605
Query	1018	TGGCCTTCAGAGGTGGCAGGAAGGGGTGAATTCCCCCTGTTGGAAAGTAATGGGAGGAGA	1077
Sbjct	2606	TGGCCTTCAGAGGTGGCAGGAAGGGGTGAATTCCCCCTGTTGGAAAGTAATGGGAGGAGA	2665
Query	1078	CTAAGGAGCTCAGGGTTGTTCTGAAGTAAAAATGCAGGCAGATGAGCATACGCTGAGT	1137
Sbjct	2666	CTAAGGAGCTCAGGGTTGTTCTGAAGTAAAAATGCAGGCAGATGAGCATACGCTGAGT	2725
Query	1138	GAGGTCCCAAGAAAAGTAACAATGGGAGCAGGTCTCAGCATAGACCTTGGTGGCGTC	1197
Sbjct	2726	GAGGTCCCAAGAAAAGTAACAATGGGAGCTGGTCTCCAGCATAGACCTTGGTGGCGTC	2785
Query	1198	CTTCTCTAGGAAGAACCTATATCTGAAGGAGCAGAAGTATTCTATCCTGCAGAACCC	1257
Sbjct	2786	CTTCTCTAGGAAGAACCTATATCTGAAGGAGCAGAAGTATTCTATCCTGCAGAACCC	2845
Query	1258	CCAGACCTCCCTGCTCTCAGAGTCTATTCCAACACCTTCAACAGGGTAAAAACGCA	1317
Sbjct	2846	CCAGACCTCCCTGCTCTCAGAGTCTATTCCAACACCTTCAACAGGGTAAAAACGCA	2905
Query	1318	GCAGAAATCTGTGAGTGGATGCCCTCTCCCAAGGTGGGATGGGTAGACCTGTGGTCAGA	1377
Sbjct	2906	GCAGAAATCTGTGAGTGGATGCCCTCTCCCAAGGTGGGATGGGTAGACCTGTGGTCAGA	2965
Query	1378	GCCCCCGGGCAGCACAGCCTAGCCGGCTCTCCCTGCAGAACCTAGAGCTGCTCCGCA	1437
Sbjct	2966	GCCCCCGGGCAGCACAGCCTAGCCGGCTCTCCCTGCAGAACCTAGAGCTGCTCCGCA	3025
Query	1438	TCTCCCTGCTGCATCCAGTCATGGCTGGACGGCCGTGCAGCTCCCTCAGGAGCTTCCG	1497

Subjct	3026	TCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCGTGCAGCTCCCTCAGGAGCGTCTCG	3085
Query	1498	CCAACAGCCTGGTATGGCGCTCGGACAGCAACGTCTATGCCACCTGAAGGACCTAG	1557
Subjct	3086	CCAACAGCCTGGTATGGCGCTCGGACAGCAACGTCTATGCCACCTGAAGGACCTAG	3145
Query	1558	AGGAAGGCATCCAACGCTGATGTGGGTGAGGGTGGCACCAAGG-ATCC--AATCTGGG	1614
Subjct	3146	AGGAAGGCATCCAACGCTGATGTGGGTGAGGGTGGCACCAAGGATCCCCAATCTGGG	3205
Query	1615	CCCCACTGGCTCCAGGGACTGGGGAGAGAACACTGCTGCCCTTTTAGCAGTCAGG	1674
Subjct	3206	CCCCACTGGCTCCAGGGACTGGGGAGAGAACACTGCTGCCCTTTTAGCAGTCAGG	3265
Query	1675	CGCTGACCCAAGAGAACTCACCGTATTCTCATTCCTCGTGAATCCTCCAGGGCTTT	1734
Subjct	3266	CGCTGACCCAAGAGAACTCACCGTATTCTCATTCCTCGTGAATCCTCCAGGGCTTT	3325
Query	1735	CTCTACAACTTGGAGGGAGGGAGGAAATGGATGAATGAGAGAGGGAGGGACAGTGCC	1794
Subjct	3326	CTCTACAACTTGGAGGGAGGGAGGAGGAAATGGATGAATGAGAGAGGGAGGGACAGTGCC	3385
Query	1795	CAAGCGCTTGGCCTCTCTTCTTCACTTGAGGGCTGGAAAGATGGCAGCCCC	1854
Subjct	3386	CAAGCGCTTGGCCTCTCTTCTTCACTTGAGGGCTGGAAAGATGGCAGCCCC	3445
Query	1855	CGGACTGGGCAGATCTCAATCAGTCCTACAGCAAGTTGACACAAAATCGCACAAAGAT	1914
Subjct	3446	CGGACTGGGCAGATCTCAATCAGTCCTACAGCAAGTTGACACAAAATCGCACAAAGAT	3505
Query	1915	GACGCACTGCTCAAGAACACTGGGCTGCTACTGCTCAGGAAGGACATGGACAAGTC	1974
Subjct	3506	GACGCACTGCTCAAGAACACTGGGCTGCTACTGCTCAGGAAGGACATGGACAAGTC	3565
Query	1975	GAGACATTCTCGCATCGTCAGTGCCTCTGTGGAGGGCAGCTGTGGCTTAGCTG	2034
Subjct	3566	GAGACATTCTCGCATCGTCAGTGCCTCTGTGGAGGGCAGCTGTGGCTTAGCTG	3625
Query	2035	CCCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCTGGTGTGGAAGGTGCTACT	2094
Subjct	3626	CCCGGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCTGGTGTGGAAGGTGCTACT	3685
Query	2095	CCAGTGCACCAACAGCCTGTCTTAATAAAATTAAAGTGCATCATTTGTTGACTAGGTG	2154
Subjct	3686	CCAGTGCACCAACAGCCTGTCTTAATAAAATTAAAGTGCATCATTTGTTGACTAGGTG	3745
Query	2155	TCTCTGTATAATATTATGGGGTGGAGGCAGGGTGGTATGGAGCAAGGGCCAGGGGGAA	2214
Subjct	3746	TCTCTGTATAATATTATGGGGTGGAGGCAGGGTGGTATGGAGCAAGGGGC-AGGTTGGAA	3804
Query	2215	GACAACCTGTAGGGCCTTCAGGGTCTATTGGAAACAGGCTGGAGTGCAGTGGCA-G-T	2272
Subjct	3805	GACAACCTGTAGGGCCTTCAGGGTCTATT-GGGAAACAGGCTGGAGTGCAGTGGCACGAT	3863
Query	2273	CTTGGCTCGCTGCAATTCGCCCTCTGGGTTCAAGCGATTCTCTGCCCTCAGTCCTCCG	2332
Subjct	3864	CTTGGCTCGCTGCAATTCGCCCTCTGGGTTCAAGCGATTCTCTGCCCTCAGTCCTCCG	3923
Query	2333	AATAGTTGCGATTCCAGGCATGCAAGAACAGGCTCAGCTAATTTGTATTTGGTAGA	2392

Subjct	3924	AATAGTGGGATTC CAGGCATGCACGACCA CAGGCTCAGCTAA TTTGTATTTGGTAGA	3983
Query	2393	GACGGGGTTTCACCATATTGGC CAGTCTGGTCTCCATCTCTGACCTCAGGTAATCCGCC	2452
Subjct	3984	GACGGGGTTTCACCATATTGGC CAGTCTGGTCTCCATCTCTGACCTCAGGTAATCCGCC	4043
Query	2453	CGCCTCGGCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTTCCCTGTCC	2512
Subjct	4044	CGCCTCGGCTCCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTTCCCTGTCC	4103
Query	2513	TGTGATTTAAAATAATTATAC CAGCAGAAGGACGTCCAGACACAGCATGGCTACCTGG	2572
Subjct	4104	TGTGATTTAAAATAATTATAC CAGCAGAAGGACGTCCAGACACAGCATGGCTACCTGG	4163
Query	2573	CCATGCCAGCCAGTGGACATTGAGTTGTTGCTGGACTGTCCCTCATGCAATTGG	2632
Subjct	4164	CCATGCCAGCCAGTGGACATTGAGTTGTTGCTGGACTGTCCCTCATGCAATTGG	4223
Query	2633	GTC CACTCAGTAGATGCTTGTGAATTC	2660
Subjct	4224	GTC CACTCAGTAGATGCTTGTGAATTC	4251

Score = 204 bits (110), Expect = 4e-49
 Identities = 213/261 (81%), Gaps = 14/261 (5%)
 Strand=Plus/Plus

Query	2250	CCAGGCTGGAGTCAGT-G-GCAGTCTGGCTCGTCGCAATCTCGCCCTCTGGGTTCAA	2307
Subjct	646	CCAGGCTGGAGTCAGTGGCCAACTTGGCTCACAGCAACCTCTGGCTCTGGGTTCAA	705
Query	2308	GCGATTCTCTGCCTCAGTCTCCGAA-TAGTTGCGATTCCAGGCA--TGCAGAACCCAGG	2364
Subjct	706	GCGATTCTCTGCCTCAGCCTCCC-AAGTAGCTGGGATTACGGGCTCGTGCCA--CCATG	762
Query	2365	-CTCAGCTAATTTGTATTTT-GGTAGAGACGGGTTTCACCATATTGGCAGTCTGG	2422
Subjct	763	AC-CAGCTAATTTGTATTTAGG-AGAGATGGAGTTTGCCATGTGGGTTAGCCTGG	820
Query	2423	TCTC-CATCTCTGCACCTCAGGTAA TCGGCCGCGCTCGGCCCTCCAAATTGCTGGGATTA	2481
Subjct	821	TCTTGCA-CTCTCGACCTTAAGTGTACCAACCCACCTCAGCCTCCAAAGTGCCTGGGATTA	879
Query	2482	CAGGTATGAGCCACTGGGCC	2502
Subjct	880	TAGGCATGAGCCACCGTGGCC	900

>emb|CS741886.1| Sequence 9882 from Patent WO2005083127
 Length=20631

Score = 4684 bits (2536), Expect = 0.0
 Identities = 2625/2670 (98%), Gaps = 16/2670 (0%)
 Strand=Plus/Minus

Query	1	GAATT CAGCACTGAATCATGCCAGAACCCCGCAATCTATTGGCTGTGCTTGGCCCT	60
Subjct	9106	GAATT CAGCACTGAATCATGCCAGAACCCCGCAATCTATTGGCTGTGCTTGGCCCT	9047

Query 61	TTCCCCAACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATGCGGGGAGGAGGAAG	120
Sbjct 9046	TTTCCCCAACACACACATTCTGTCTGGTGGGTGGAGGGGAAACATGCGGGGAGGAGGAAG	8987
Query 121	GAATAGGATAGAGAGTGTTGGGTGGGTCTCAAGGACTGGCCTATCCTGACA	180
Sbjct 8986	GAATAGGATAGAGAGTGTTGGGTGGGTCTCAAGGACTGG-CTATCCTGACA	8928
Query 181	TCTCTTCGGCGTTCAGGTGGGCCACCATGGCCTGCTGCCAGAGGGCACCCACGTGACCC	240
Sbjct 8927	TCTCTTCGGCGTTCAGGTGGGCCACCATGGCCTGCTGCCAGAGGGCACCCACGTGACCC	8868
Query 241	TTAAAGAGAGGACAAGTTGGTGGTATCTCT-GCTGACATTCTGTGACAACCCCTACAA	300
Sbjct 8867	TTAAAGAGAGGACAAGTTGGTGGTATCTCT-GCTGACATTCTGTGACAACCCCTACAA	8809
Query 301	CGCTGGTGTGGTGGGAAGGGAAAGATGACAAGTCAGGGGCATGATCCCAGCATGTGTG	360
Sbjct 8808	CGCTGGTGTGGTGGGAAGGGAAAGATGACAAGTCAGGGGCATGATCCCAGCATGTGTG	8749
Query 361	GGAGGAGCTCTAAATTATCATTAGACAAGCCGTCACTGGCCCAGGCCCTAACATG	420
Sbjct 8748	GGAGGAGCTCTAAATTATCATTAGACAAGCCGTCACTGGCCCAGGCCCTAACATG	8689
Query 421	CAGAGAACAGGTGAGGAGAACGAGCGAGAGAGAACGGGCCAGGTATAAAAGGGCCAC	480
Sbjct 8688	CAGAGAACAGGTGAGGAGAACGAGCGAGAGAACGGGCCAGGTATAAAAGGGCCAC	8629
Query 481	AAGAGACCAGCTCAAGGATCCAAAGGCCAACCTCCGAAACCACCTAGGGTCTGTGGAC	540
Sbjct 8628	AAGAGACCAGCTCAAGGATCCAAAGGCCAACCTCCGAAACCACCTAGGGTCTGTGGAC	8569
Query 541	AGCTCA-CTAGCGGCAATGGTGTGAGGTAAAGGCCCTAAATCCCTT-GGCACATGT	598
Sbjct 8568	AGCTCACCTAGCGGCAATGGTGTGAGGTAAAGGCCCTAAATCCCTTGGGCACATGT	8509
Query 599	GTCTTGAGGGGAGAGCGCGCTCTGTAGATGGGACGGGGCACTAACCTCAGGTTGG	658
Sbjct 8508	GTCTTGAGGGGAGAGCGCGCTCTGTAGATGGGACGGGGCACTAACCTCAGGTTGG	8449
Query 659	GGCTTATGAATGTTAGTATCGCCATCTAACGCCAGTATTGGCCATCTGAATGTT	718
Sbjct 8448	GGCTTATGAATGTTAG-TATGCCATCTAACGCCAGTATTGGCCATCTGAATGTT	8390
Query 719	CTGGTCCCTGGA-GGAGGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	777
Sbjct 8389	CTGGTCCCTGGAGGGAGGC-AGAGAGAGAGAGAGARAAAAAAACCCAGCTCTGGAAC	8331
Query 778	AGGGAGAGCGCTGGCTTCTCCAGCTCCCTGTG-CCTCCGGTTCTCCCCAG	836
Sbjct 8330	AGGGAGAGCGCTGGCTTCTCCAGCTCCCTGTG-CCTCCGGTTCTCCCCAG	8271
Query 837	GCTCCCGAGCTCCCTGTCTGGCTTTGGCCTGCTCTGCCAGCTCCCTGTG-CCTCCGGTTCTCCCCAG	896
Sbjct 8270	GCTCCCGAGCTCCCTGTCTGGCTTTGGCCTGCTCTGCCAGCTCCGGTTCTCCCCAG	8211
Query 897	GCAGTGCCTTCCAACCATTCCCTTATCCAGGCTTTTGACAACGCTATGCTCCGGCC	956
Sbjct 8210	GCAGTGCCTTCCAACCATTCCCTTATCCAGGCTTTTGACAACGCTATGCTCCGGCC	8151

Query	957	GTCGCCTGTACCAAGCTGGCATATGACACCTATCAGGAGTTGTAAGCTTGGGTAATGG	1016
Sbjct	8150	GTCGCCTGTACCAAGCTGGCATATGACACCTATCAGGAGTTGTAAGCTTGGGTAATGG	8091
Query	1017	GTGCGCTTCAGAGGTGGCAGGAAGGGGTGAATTCCCCCGCTGGGAAGTAATGGGAGGAG	1076
Sbjct	8090	GTGCGCTTCAGAGGTGGCAGGAAGGGGTGAMTTCCCCCGCTGGGAAGTAATGGGAGGAG	8031
Query	1077	ACTAAGGAGCTCAGGGTTGTTCTGAAGTAAAAATGCAGGCAGATGAGCATACGCTGAG	1136
Sbjct	8030	ACTAAGGAGCTCAGGGTGTTCTGAAGTAAAAATGCAGGCAGATGAGCATACGCTGAG	7971
Query	1137	TGAGGTTCCCAAGAAAAGTAACATGGGAGCAGGGCTCCAGCATAGACCTTGGTGGCGGT	1196
Sbjct	7970	TGAGGTTCCCAAGAAAAGTAACATGGGAGCAGGGCTCCAGCATAGACCTTGGTGGCGGT	7911
Query	1197	CCTTCTCTAGGAAAGAACCTATATCCTGAAGGAGCAGAAGTATTCTTCAGAAC	1256
Sbjct	7910	CCTTCTCTAGGAAAGAACCTATATCCTGAAGGAGCAGAAGTATTCTTCAGAAC	7851
Query	1257	CCCAGACCTCCCTCTGCTCTCAGAGTCTATTCCAACACCTTCAACAGGGTAAAAACGC	1316
Sbjct	7850	CCCAGACCTCCCTCTGCTCTCAGAGTCTATTCCAACACCTTCAACWGGGTAAAAACGC	7791
Query	1317	AGCAGAAATCTGTGAGTGGATGCCCTCTCCCAGGT-GGGATGGGTAGACCTGTGGTCA	1375
Sbjct	7790	AGCAGAAATCTGTGAGTGGATGCCCTCTCCCAGGTGGGTAGGGTAGACCTGTGGTCA	7731
Query	1376	GAGCCCCGGGCAGCACAGCCTAGCCGCTTCTCCCTCGCAGAACCTAGAGCTGCCCG	1435
Sbjct	7730	GAGCCCCGGGCAGCACAGCCTAGCCGCTTCTCCCTCGCAGAACCTAGAGCTGCCCG	7671
Query	1436	CATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCCTGCAGCTCTCAGGAGCTCTT	1495
Sbjct	7670	CATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCCCTGCAGCTCTCAGGAGCTCTT	7611
Query	1496	CGCCAACAGCCTGGTGTATGGCGCTCGGACAGCAACGTCATGCCACCTGAAGGACCT	1555
Sbjct	7610	CGCCAACAGCCTGGTGTATGGCGCTCGGACAGCAACGTCATGCCACCTGAAGGACCT	7551
Query	1556	AGAGGAAGGCATCCAAACGCTGATGGTGGGTGAGGGTGGCACCA-GGAT--CCAACTCTGG	1612
Sbjct	7550	AGAGGAAGGCATCCAAACGCTGATGGTGGGTGAGGGTGGCACCAAGGGATCCCAACTCTGG	7491
Query	1613	GGCCCCACTGGCTCCAGGGACTGGGAGAGAAACACTGCTGCCCTTTAGCAGTC	1672
Sbjct	7490	GGCCCCACTGGCTCCAGGGACTGGGAGAGAAACACTGCTGCCCTTTAGCAGTC	7431
Query	1673	GGCGCTGACCCAAGAGAACTCACCGTATTCTCATTCCTCGTGAATCTCCAGGCCT	1732
Sbjct	7430	GGCGCTGACCCAAGAGAACTCACCGTATTCTCATTCCTCGTGAATCTCCAGGCCT	7371
Query	1733	TTCTCTACAAACCTGGAGGGAGGGAGGAAATGGATGAATGAGAGAGGGAGGGAACAGTG	1792
Sbjct	7370	TTCTCTACAAACCTGRAGGGGRGGGAGGAAATGGATGAATGAGAGAGGGAGGGAACAGTG	7311
Query	1793	CCCAAGCGCTTGGCCTCTCCTCTTCACTTGCAGAGGCTGGAAGATGGCAGCC	1852
Sbjct	7310	CCCAAGCGCTTGGCCTCTCCTTCACTTGCAGAGGCTGGAAGATGGCAGCC	7251

Query	1853	CCCGGACTGGGCAGATCTCAATCAGTCTACAGCAAGTTGACACAAAATCGCACAAACG	1912
Sbjct	7250	CCCGGACTGGGCAGATCTCAATCAGTCTACAGCAAGTTGACACAAAATCGCACAAACG	7191
Query	1913	ATGACGCACTGCTCAAGAACTACGGGCTGCTACTGCTTCAGGAAGGACATGGACAAGG	1972
Sbjct	7190	ATGACGCACTGCTCAAGAACTACGGGCTGCTACTGCTTCAGGAAGGACATGGACAAGG	7131
Query	1973	TGAGACATTCCTCGCGATCGTCAGTCCGCTCTGGAGGGCAGCTGTGGCTCTAGC	2032
Sbjct	7130	TGAGACATTCCTCGCGATCGTCAGTCCGCTCTGGAGGGCAGCTGTGGCTCTAGC	7071
Query	2033	TGCCCCGGTGGCATCCCTGTGACCCCTCCCCAGTCGCTCTCCCTGGCTGTGGAAGGTGCTA	2092
Sbjct	7070	TGCCCCGGTGGCATCCCTGTGACCCCTCCCCASTGCCTCTCCCTGGTSGTGGAAAGGTGCTA	7011
Query	2093	CTCCAGTGCCACCAGCCTTGTCTTAATAAAATTAAGTGTGATCATTTGTTGACTAGG	2152
Sbjct	7010	CTCCAGTGCCACCAGCCTTGTCTTAATAAAATTAAGTGTGATCATTTGTTGACTAGG	6951
Query	2153	TGTCCTTGATAATATTATGGGGTGGAGCGGGTGGTATGGAGCAAGGGGCAGTTGG	2212
Sbjct	6950	TGTCCTTGATAATATTATGGGGTGGAGCGGGTGGTATGGAGCAAGGGG-CAGTTGG	6892
Query	2213	AAGACAAACCTGTAGGGCCTTCAGGGTCTATTGGGAACCAGGCTGGAGTGCAGTGGCA-G	2271
Sbjct	6891	AAGACAAACCTGTAGGGCCTTCAGGGTCTATT-GGGAACAGGCTGGAGTGCAGTGGCACG	6833
Query	2272	-TCTTGCTCGCTGCAATCTCCGCTCTGGTTCAAGCGATTCTCTGCTCAGTCCTC	2330
Sbjct	6832	ATCTTGCTCGCTGCAATCTCCGCTCTGGTTCAAGCGATTCTCTGCTCAGTCCTC	6773
Query	2331	CGAATAGTTGCGATTCAGGCATGCAAGACCAGGCTCAGCTAATTTGTATTTGGTA	2390
Sbjct	6772	CGAATAGTTGGGATTCAGGCATGCAAGACCAGGCTCAGCTAATTTGTATTTGGTA	6713
Query	2391	GAGACGGGTTTACCATATTGCCAGTCTGGTCTCCATCTCTGACCTCAGGTAATCCG	2450
Sbjct	6712	GAGACGGGTTTACCATATTGCCAGTCTGGTCTCCATCTCTGACCTCAGGTAATCCG	6653
Query	2451	CCGCCTCGCCCTCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTCCCTGT	2510
Sbjct	6652	CCGCCTCGCCCTCCAAATTGCTGGGATTACAGGTATGAGCCACTGGGCCCTCCCTGT	6593
Query	2511	CCTGTGATTTAAATAATTATACCAGCAGAAGGACGTCCAGACACAGCATGGCTACCT	2570
Sbjct	6592	CCTGTGATTTAAATAATTATACCAGCAGAAGGACGTCCAGACACAGCATGGCTACCT	6533
Query	2571	GGCATGCCAGCCAGTGGACATTGAGTTGCTGGACTGTCTCATGCTT	2630
Sbjct	6532	GRCCATGCCAGCCAGTGGACATTGAGTTGCTGGACTGTCTCATGCTT	6473
Query	2631	GGGTCCACTCAGTAGATGCTTGTGAATTC	2660
Sbjct	6472	GGGTCCACTCAGTAGATGCTTGTGAATTC	6443

Score = 1037 bits (561), Expect = 0.0
 Identities = 680/737 (92%), Gaps = 9/737 (1%)
 Strand=Plus/Minus

Query 1	GAATTCA GCACTGAATCATGCCAGAACCCCCGCAATCTATTGGCTGTGCCTTGGCCCT	60
Sbjct 952	GAATTCA GAGACTCAATGGTGCTCAGAACCCCCCACAACTATTGGCTGTGC-TTGGCCCT	894
Query 61	TTTCCCACACACACATTCTGCTGGTGGGTGGGGAAACATGCGGGGAGGAGGAAAG	120
Sbjct 893	TTTCCCACACACACATTCTGCTGGTGGGTGGAAAGTTAACACCGCGGGAGGAGGAAAG	834
Query 121	GAATAGGATAGAGAGTGGGATGGGTGGTAGGGCTCAAGGACTGGCTATCCTGACA	180
Sbjct 833	GAATAGGATAGAGAGTGGAAATGGGTGGTAGGGCTCAAGGACTGG-CTATCCTGACA	775
Query 181	TCTTCTCCGGTTCAGGTTGCCACCATGGCTGCTGCCAGAGGGCACCCACGTGACCC	240
Sbjct 774	GCCTTC CCCC GGTT CAGGTTGACCAACATGGCTGCGACCCAGAGGGCACCCACGTGACCC	715
Query 241	TTAAAGAGAGGACAAGTTGGGTGTA-TCTCTGGCTGACATTCTGTGACAACCCCTACA	299
Sbjct 714	TTAAAGAGAGGACAAGTTGGTGAGTGTGAG-AGTCTGTGGCTGACACTCTGTGACAATCCTTACA	656
Query 300	ACGCTGGTGATGGTGGGAAGGGAAAGATGACAAGTCAGGGGGCATGATCCCAGCATGTGT	359
Sbjct 655	ACACTGGTGATGGTGAGAAGGGAAAGACGACAAGCCAGGGGCATGATCCCAGCATGTGT	596
Query 360	GGGAGGGAGCTCTAAATTATCATTAGCACAAAGCCCGTCAGTGGCCCCAGGGCTAAACAT	419
Sbjct 595	GGGAGGGAGCTCCAATTATCATTAGCACAAAGCCCGTCAGTGGCCCCATGCATAAATGT	536
Query 420	GCAGAGAAAACAGGTGAGGAGAACGCAGCGAGAGAGAAGGGGCCAGG-TATAAAAGGCC	478
Sbjct 535	ACACAGAAAACAGGTGGGTCAAGCAGGGAGAGAGAACTGGCAGGGTATAAAAGGCC	476
Query 479	ACAAGAGACCAGCTCAAGGATCCCAAGGCCAACACTCCCGAACCACTCAGGGTCTGTGG	538
Sbjct 475	ACAAGAGACCAGCTCTAGGATCCCAAGGCCAACACTCCCGAACCACTCAGGGTCTGTGG	416
Query 539	ACAGCTCAC-TAGCGCAATGCCATCAGGTAAGCCCTAAATCCCTTGG-CACAAAT	596
Sbjct 415	ACAGCTCACCTAGGGCAATGCCATCAGGTAAGCCCTAAATCCCTTGGCACAAAC	356
Query 597	GTGT CCTGAGGGGAGAGCGCCGCTCTGTAGATGGACGGGGCACTAACCTCAGGTT	656
Sbjct 355	GTGT CCTGAGGGGAGAGCGCCGCTGTAGATGGACGGGGCACTAACCTCAGGTT	296
Query 657	GGGGCTTATGAATGTTAGCTATGCCATCTAACGGCCAG-TATTTGGCAATCTGTGAATG	715
Sbjct 295	GGGGCTTATGAATGTGAG-TATGCCATCTAACGGCCAGATATTGGCAATCTGTGAATG	237
Query 716	TCCTGGCTCCCTGGAGG 732	
Sbjct 236	TCCTGGTCTCTGGAGG 220	
Score = 255 bits (138), Expect = 1e-64		
Identities = 172/188 (91%), Gaps = 3/188 (1%)		
Strand=Plus/Minus		
Query 765	CAGCTCCTGGAACAGGGAGAGCGCTGGCCTCTGGCTCCAGCTCCCTGTG-CCTCC	823

Sbjct	194	CAGCTCCTGGAGCAGGGAGAGCGCTGGCCTTCCTCTCCGGCTCCCTCATTGCCCTCC	135
Query	824	GGTTTCTCCCAAGGCTCCCGGACGTGCTGGCTTGCCTGGCTTGCCTGCTGCTGTCC 	883
Sbjct	134	GGTTTCTCCCAAGGCTCCCGGACGTGCTGGCTTGCCTGGCTTGCCTGCTGCTGCC	75
Query	884	TGGCTTCAAGAGGGCAG-TGCCTCCCAACCATTCCCTATCCAGGGCTTTGACAACGC 	942
Sbjct	74	TGGCTTCAAGAGG-CTGGTGCGTCCAAACCGTCCGTTATCCAGGGCTTTGACCAACGC	16
Query	943	TATGCTCC 950 	
Sbjct	15	TATGCTCC 8	
<p>Score = 209 bits (113), Expect = 8e-51 Identities = 213/260 (81%), Gaps = 12/260 (4%) Strand=Plus/Minus</p>			
Query	2250	CCAGGCTGGAGTGCAGT-G-GCAGTCTGGCTCGCTGCAATCTCCGCCCTGGGTCAA 	2307
Sbjct	10049	CCAGGCTGGAGTGCAGTGGCGCAATCTGGCTCACAGAACCTTGCCCTGGGTCAA	9990
Query	2308	GCGATTCTCTGCCTCAGTCTCCGAA-TAGTTGCGATTCCAGGCA--TGCAAGACCAGG 	2364
Sbjct	9989	GCGATTCTCTGCCTCAGCCTCCC-AAGTAGCTGGATTACGGGCTCGGCCA--CCATG	9933
Query	2365	CTCAGCTAATTTGTATTTT-GGTAGAGACGGGTTTCACCATATTGGCCAGTCTGGT 	2423
Sbjct	9932	CCCAGCTAATTTGTATTTAGG-AGAGATGGAGTTTGCATGTGGGTTAGCCTGGT	9874
Query	2424	CTC-CATCTCCGACCTCAGGTAAATCGGCCGCCCTCGGCCCTCCAAATTGCTGGGATTAC 	2482
Sbjct	9873	CTTGCA-CTCTGACCTTAAGTGTACCCACCTCAGCCTCCAAAGTGTGGGATTAT	9815
Query	2483	AGGTATGAGCCACTGGGCC 2502 	
Sbjct	9814	AGGCATGAGCCACCGTGC 9795	

>emb|CS741885.1| Sequence 9881 from Patent WO2005083127
 Length=58905

Score = 4684 bits (2536), Expect = 0.0
 Identities = 2625/2670 (98%), Gaps = 16/2670 (0%)
 Strand=Plus/Plus

Query	1	GAATTCACTGAATCATGCCAGAACCCCCGCAATCTATTGGCTGTGCTTGGCCCT 	60
Sbjct	42593	GAATTCACTGAATCATGCCAGAACCCCCGCAATCTATTGGCTGTGCTTGGCCCT	42652
Query	61	TTTCCCAACACACATCTGCTGGGGTGGAGGGGAAACATCGGGGGAGGAGGAAAG 	120
Sbjct	42653	TTTCCCAACACACATCTGCTGGGGTGGAGGGAAACATCGGGGGAGGAGGAAAG	42712
Query	121	GAATAGGATAGAGAGTGGGATGGGTGGTCTCAAGGACTGGCTATCTGACA 	180
Sbjct	42713	GAATAGGATAGAGAGTGGGATGGGTGGTCTCAAGGACTGG-CTATCTGACA	42771
Query	181	TCCCTCTCCGCGTTCAAGGTGGCCACCATGGCCCTGCGCAGAGGGCACCCACGTGACCC 	240

Sbjct	42772	TCCTCTCCGCGTTCAGGTTGCCACCATGGCTGCTGCCAGAGGGACCCACGTGACCC	42831
Query	241	TTAAGAGAGGACAAGTGGGTGATCTCTGGCTGACATTCTGTGCAACACCTCACA	300
Sbjct	42832	TTAAGAGAGGACAAGTGGGTGATCTCT-GCTGACATTCTGTGCAACACCTCACA	42890
Query	301	CGCTGGTGTGGAAAGGGAAAGATGACAAGTCAGGGGCATGATCCCAGCATGTG	360
Sbjct	42891	CGCTGGTGTGGAAAGGGAAAGATGACAAGTCAGGGGCATGATCCCAGCATGTG	42950
Query	361	GGAGGAGCTCTAAATTATCATTAGCACAAAGCCCGTCAGTGGCCCAGGCCTAAACATG	420
Sbjct	42951	GGAGGAGCTCTAAATTATCATTAGCACAAAGCCCGTCAGTGGCCCAGGCCTAAACATG	43010
Query	421	CAGAGAACAGGTGAGGGAGAGCAGCGAGAGAGAGAGGGGCCAGGTATAAAAGGGCCAC	480
Sbjct	43011	CAGAGAACAGGTGAGGGAGAGCAGCGAGAGAGAGGGGCCAGGTATAAAAGGGCCAC	43070
Query	481	AAGAGACCAGCTAAGGATCCAAGGCCAACTCCCCAACCACTCAGGGTCTGTGGAC	540
Sbjct	43071	AAGAGACCAGCTAAGGATCCAAGGCCAACCACTCCCCAACCACTCAGGGTCTGTGGAC	43130
Query	541	AGCTCA-CTAGCGGAATGGCTGCAGGTAAGCGCCCCCTAAATCCCTT-GGCACAAATGT	598
Sbjct	43131	AGCTCACCTAGCGGAATGGCTGCAGGTAAGCGCCCCCTAAATCCCTTGGCACAAATGT	43190
Query	599	GTCTCTGAGGGGAGAGGCCGCGCTCTGTAGATGGACGGGGCACTAACCTCAGGTTTG	658
Sbjct	43191	GTCTCTGAGGGGAGAGGCCGCGCTCTGTAGATGGACGGGGCACTAACCTCAGGTTTG	43250
Query	659	GGCTTATGAATGTTAGCTATGCCATCTAACCCAGTATTGGCAATCTGAATGTT	718
Sbjct	43251	GGCTTATGAATGTTAG-TATGCCATCTAACCCAGTATTGGCAATCTGAATGTT	43309
Query	719	CTGGTCCCTGGA-GGAGGCAagagagagagagagaaaaaaaACCAAGCTCTGGAAC	777
Sbjct	43310	CTGGTCCCTGGAGGGAGGC-AGAGAGAGAGAGARAAAAAAACCCAGCTCTGGAAC	43368
Query	778	AGGGAGAGCGCTGGCTCTTGTCTCCAGCTCCCTCTGTT-GCTCCGTTCTCCCAAG	836
Sbjct	43369	AGGGAGAGCGCTGGCTCTTGTCTCCAGCTCCCTCTGTTGCCCTCCGTTCTCCCAAG	43428
Query	837	GCTCCCGGACGTCCCTGCTCTGGCTTTGCCCTGCTCTGCCCTGGCTCAAGAGG	896
Sbjct	43429	GCTCCCGGACGTCCCTGCTCTGGCTTTGCCCTGCTCTGCCCTGGCTCAAGAGG	43488
Query	897	GCAGTGCCTTCCAACCATCCCTTACAGGCTTTGACAACGCTATGCTCCGCGCCC	956
Sbjct	43489	GCAGTGCCTTCCAACCATCCCTTACAGGCTTTGACAACGCTATGCTCCGCGCCC	43548
Query	957	GTGCCCTGTACCAAGCTGGCATATGACACCTATCAGGAGTTGTAAGCTTGGTAATGG	1016
Sbjct	43549	GTGCCCTGTACCAAGCTGGCATATGACACCTATCAGGAGTTGTAAGCTTGGTAATGG	43608
Query	1017	GTGCGCTTCAGAGGTGGCAGGAAGGGTGAATTCCCGCTGGGAAGTAATGGAGGAG	1076
Sbjct	43609	GTGCGCTTCAGAGGTGGCAGGAAGGGTGAATTCCCGCTGGGAAGTAATGGAGGAG	43668
Query	1077	ACTAAGGGAGCTCAGGGTTTCTGAAGTAAAATGAGCAGGAGATGAGCATACGCTGAG	1136

Score = 2760 bits (1494), Expect = 0.0
Identities = 1766/1908 (92%), Gaps = 19/1908 (0%)
Strand=Plus/Plus

Query	765	CAGCTCTGGAAACAGGGAGAGCCTGGCTCCAGCTCCCTCTGTG-CCTCC	823
Sbjct	6412	CAGCTCTGGAGCAGGGAGAGYGTGGCTCCGCTCCCTGTGTCGCCCT	6471
Query	824	GGTTCTCCCCAGGCTCCGGACGTCCCTGCTCCGGCTTTGGCTGCTCGCTGTCC	883
Sbjct	6472	GGTTCTCCCCAGGCTCCGGACGTCCCTGCTCCGGCTTTGGCTGCTCGCTGCC	6531

Query	884	TGGCTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTATCCAGGCTTTGACAACGCT	943
Sbjct	6532	TGGCTTCAAGAGGGCAGTGCCTTCCCAACCATTCCCTATCCAGGCTTTGACAACGCT	6591
Query	944	ATGCTCGCGCCGCTCGCCTGTACAGCTGGCATATGACACCTATCAGGAGTTGAAAGC	1003
Sbjct	6592	ATGCTCYGCGCCATCGCTGCACCAGCTGGCMTWTGACAYCTACAGGAGTTGTAAGC	6651
Query	1004	TCTTGGGTAATGGGTGCGCTCAGAGGTGGCAGGAAGGGTGAATTCCCCCGCTGGAA	1063
Sbjct	6652	TCTTGGGATGGGTGCGCATCAGGGTGGCAGGAAGGGTGAATTCCCCCGCTGGAA	6711
Query	1064	GTAATG-GGAGGAGACTAAGGGAGCTCAGGGTTGTTCTGAAGTGAAGTGCAGGAGAT	1122
Sbjct	6712	ATAA-GAGGAGGAGACTAAGGGAGCTCAGGGTT-TTCCYGAAGCGAAAATGCAGGAGAT	6769
Query	1123	GAGCATACTGCTGAGTGAGGTCCCGAAGAAAGTAACAATGGGAGCAGGTCTCCAGCATAGA	1182
Sbjct	6770	GAGCACACGCTGAGTGAGGTCCCGAAGAAAGTAACAATGGGAGCTGGTCTCCAGCGTAGA	6829
Query	1183	CCTTGGTGGCGGTCTCTCTAGGAAGAACCTATATCTGAAGGAGCAGAAGTATTG	1242
Sbjct	6830	CCTTGGTGGCGGTCTCTCTAGGAAGAACCTATATCCAAAGGAACAGAAGTATTG	6889
Query	1243	ATTCCTGCAGAACCCCCAGACCTCCCTCTGCTTCTCAGAGTCTATTCAAACACCTCCAA	1302
Sbjct	6890	ATTCCTGCAGAACCCCCAGACCTCCCTCTGTTCTCAGAGTCTATTCCGACACCTCCAA	6949
Query	1303	CAGGGTGAACACGCAAGCAAAAT-CTGTGAGTGGATGCCTTCTCCCAGG-TGGGATGGG	1360
Sbjct	6950	CAGGGAGGAACACAAACAGAAATYC-CTGAGTGGATGCCTTCTCCCAGGCGGGATGGG	7008
Query	1361	GTAGACCTGTGGTCAGAGCCCCCGGGCAGCACAGCCACTGCCGTCTTCCCAGAA	1420
Sbjct	7009	GGAGACCTGTAGTCAGAGCCCCCGGGCAGCACAGCAAATGCCGTCTTCCCAGAA	7068
Query	1421	CCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGCCGTGCAGCT	1480
Sbjct	7069	CCTARAGCTGCTCYGCATCTSCCTGCTGCTCATCCAGTCAGTCAGTGGAGCCGTGCAGTT	7128
Query	1481	CCTCAGGAGCGTCTCGCAACAGCTGGTGTATGGCGCTCGAGCACAGCAACGCTATCG	1540
Sbjct	7129	CCTCAGGAGTGTCTCGCAACAGCTGGTGTACCGCGCTCTGCAWGCAACDCTCAT-G	7187
Query	1541	-CCACCTGAAGGACCTAGAGGAAGGCATCAAACGCTGATGGGGTGGAGGGACCAAA-	1598
Sbjct	7188	RCCTCTAAAGGACCTAGAGGAAGGCATCAAACRCTGATGGGGTGGAGGGTGGCCAG	7247
Query	1599	GGAT--CCAATCTGGGGCCCCACTGGCTTCCAGGGACTG-GGGAGAGAAACACTGCTGC	1655
Sbjct	7248	GGKTCCCCATCTGGAGCCCCACTGACTTTGAGAG-CTGTRTTAGAGAAACACTGCTGC	7306
Query	1656	CCTTTTTAGCAGTCAGGCCTGACCCAAAGAGAACTCACCGTATTCTCATTCCTC	1715
Sbjct	7307	CCTTTTTAGCAGWCAGGCCCTGACCCAAAGAGAACTCACCTTATCTCATTCCTC	7366
Query	1716	GTGAATCCTCCAGGCCCTTCTACAACTGGAGGGAGGGAGGGAAAATGGATGAATGAG	1775
Sbjct	7367	RTGAATCCTCCAGGCCWTTCTACACCTGAAGGGAGGGAGGGAAAATGAATGAATGAG	7426

Query	1776	AGAGGGAGGGAAACAGTGCCAAGCGTGGCTCTCCTCTTCACTTGCAGAG	1835
Sbjct	7427	AAAGGGAGGGAAACAGTACCCAAGCGTGGCTCTCCTCTTCACTTGCAGAG	7486
Query	1836	GCTGGAAGATGGCAGCCCCCGACTGGGCAGATCTCAATCAGTCTACAGCAAGTTGA	1895
Sbjct	7487	GCTGGAAGATGGCAGCCCCCGACTGGGCAGATCTCAAGCAGACCTACAGCAAGTTGA	7546
Query	1896	CACAAAATCGCACAACGATGACGCAGTGCCTCAAGAACATCAGGCTGCTACTGCTTCAG	1955
Sbjct	7547	CACAAAATCRCACAACGATGACGCAGTCTCAAGAACATCAGGCTGCTACTGCTTCAG	7606
Query	1956	GAAGGGACATGGACAAGGTCGAGACATTCTCGCAGTCAGTGCCGCTCTGTGGAGGG	2015
Sbjct	7607	GAAGGGACATGGACAAGGTCGAGACATTCTCGCAGTCAGTGCCGCTCTGTGGAGGG	7666
Query	2016	CAGCTGTGGCTCTAGCTGCCCGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCCT	2075
Sbjct	7667	CAGCTGTGGCTCTAGCTGCCCGGTGGCATCCCTGTGACCCCTCCCCAGTGCCTCTCCT	7726
Query	2076	GGTCGTGAAAGGTGCTACTCCAGTGCCACCAGCCTGTCTAAATAAAATTAAGTGCAT	2135
Sbjct	7727	GGCCCTGGAAGTTGCCACTCCAGTGCCACCAGCCTGTCTAAATAAAATTAAGTGCAT	7786
Query	2136	CATTTGTTGACTAGGTGTCTTGTATAATATTATGGGGTGGAGGCGGGTGGTATGGAG	2195
Sbjct	7787	CATTTGTCGACTAGGTGTCTTGTATAATATTATGGGGTGGAGGAGGGGGTGGTATGGAG	7846
Query	2196	CAAGGGGCCAGGGTGGAAAGACAACCTGTAGGGCCTTCAGGGTCTATTGGGAAACCCAGGC	2255
Sbjct	7847	CAAGGGGCCAAG- TTGGGAAAGACAACCTGTAGGGCCTTCAGGGTCTATT-GGGAAACCAAGC	7904
Query	2256	TGGAGTGCAGTGGCAG--TCTTGGCTCGCTGCAATCTCCGCTCTGGGTTCAAGCGATT	2313
Sbjct	7905	TGGAGTGCAGTGGCACAATCTGGCTACTGCAATCTCCGCTCTGGGTTCAAGCGATT	7964
Query	2314	CTCCCTGCCCTCAGTCCTCCGAATAGTGGCATTCCAGGCATGCAAGAACCCAGGCTCAGCTAA	2373
Sbjct	7965	CTCCCTGCCCTCAGCCTCCCGAGTGGGATTCCAGGCATGCAAGAACCCAGGCTCAGCTAA	8024
Query	2374	TTTTGTATTTGGTAGAGACGGGGTTTCACCATATTGGCCAGTCTGGTCTCCATCTCC	2433
Sbjct	8025	TTTTGTATTTGGTAGAGACGGGGTTTCACCATATTGGCCAGGCTGGTCTCCAACTCC	8084
Query	2434	TGACCTCAGGTAACTGCCCGCCTCGGCCTCCAAATTGCTGGGATTACAGGTATGAGCC	2493
Sbjct	8085	TAATCTCAGGTGATCTACCCACCTGGCCTCCAAATTGCTGGGATTACAGGCGTAACC	8144
Query	2494	ACTGGGCCCTCCCTGTCTG-TGATTTAAAAAATTATACCAAGCAGAAGGACGTCAG	2552
Sbjct	8145	ACTGCTCCCTCCCTGTCTGATTTAAAAAATTATACCAAGCAGGAGGACGTCAG	8204
Query	2553	ACACAGCATGGCTACCTGGCAGTCCCAGCCAGTGGCAGATTGAGTTGCTTGGC	2612
Sbjct	8205	ACACAGCATGGCTACCTGGCAGTCCCAGCCAAACGGTGGGACATTGAGTTGCTTGGC	8264
Query	2613	ACTGTCTCTCATGCATGGGTCACACTAGTAGATGCTTGAATT	2660
Sbjct	8265	ACTGTCTCTCATGCATGGGTCACACTAGTAGATGCTTGAATT	8312

Score = 1940 bits (1050), Expect = 0.0
 Identities = 1367/1518 (90%), Gaps = 39/1518 (2%)
 Strand=Plus/Plus

Query 765	CAGCTCCCTGGAACAGGGAGAGCGCTGGCCCTCTGCTCTCCAGCTCCCTGTG-CCTCC	823
Sbjct 28671	CAGCTCCCTGGAGCAGGGAGAGCGCTGGCCCTCTCCTCTCCAGCTCCCTGTG-CCTCC	28730
Query 824	GGTTTCTCCCCAGGGCTCCCGAACGCTCCCTGCTCTGGCTTGGCTGCTCTGCCGTGCCC	883
Sbjct 28731	GGTTTCTCCCCAGGGCTCCCGAACGCTCCCTGCTCTGGCTTGGCTGCTCTGCCGTGCCC	28790
Query 884	TGGCTTCAAGAGGGC-AAGTCTCTCCCAACCCATTCCCTTATCAGGCTTTTGACAAACGC	942
Sbjct 28791	TGGCTTCAAGA-GGCTGGTGCCTCAAACCGTTCCTGTTATCAGGCTTTTGACACACGC	28849
Query 943	TATGCTCCCGGCCGTCGC-CTGTACAGCTGG-CATATGACACCTATCAGGAGTTGTA	1000
Sbjct 28850	TATGCTCCAAGGCCATCGCGC-GCACCGCTGGCCAT-TGACACCTACCAGGAGTTGTA	28907
Query 1001	AGCTTGGGATAATGGGTGCGCTTACAGGGTGGCAGGAAGGGGTTGAATTCCTCCCGT-G	1059
Sbjct 28908	AGTTCTGGGAAATGGGTGCGGGTCAGGGGTTGCAAGAAGGGGTTGACTTCCCCACTGG	28967
Query 1060	GGAAGTAATGGGAGGGAGACTAAGGAGCTCAGGGTTGTTTCTGAAGTAAAAATGCAGGCA	1119
Sbjct 28968	GGAAGTAATGGGAGGGAGACTAAGGAGCTCAGGGTTGTTTCTGAAGCAGAAAATGCAGGCA	29027
Query 1120	GATGAGCATACTGAGTGAGTTCCCAGAAAAGTAACAATGGAGCAGGTCTCAGCAT	1179
Sbjct 29028	GATGAGCATAAGGTGAGCCAGTTCCCAGAAAAGCAACAATGGAGCTGGCTCCAGCAT	29087
Query 1180	-----AG-A---C---CTTGGTGGGGCGGTCCCTCTCTAGGAAGAAGCCTATATCTGA	1226
Sbjct 29088	AGAAACCGACAGCTCTTCTTGGTGGGGGTCTCTCTAGGAAGAAAACCTATATCCAA	29147
Query 1227	AGGAGCAGAAAGTATTCTTCTGCAGAACCCCCAGACCTCCCTCTGCTCTCAGAGTCT	1285
Sbjct 29148	AGGACCCAGAAAGTATTCTTCTGCAGT-ACCTCCAGACCTCTCTGCTCTCAGACTCT	29206
Query 1286	ATTCCAACACCTTCAACAGGGTGAACAGCAGCAGAAATCTGTGAGTGGATGCCCTCTC	1345
Sbjct 29207	ATTCCGACACCCCTCAACATGGAGAACGCACAGAAATCCGTGAGTGGATGCCGTCTC	29266
Query 1346	CCC-AGG-TGGGTGGGGTAGACCTGTGGTCAGAGCCCCGGGGCAGCACAGCCACTGCC	1403
Sbjct 29267	CCCTAGGCGGGGATGGGGAGACCTGTGGTCAGGGCTCCGGCAGCACAGCCACTGCC	29326
Query 1404	GTCCCTCCCCCTGCAAGAACCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCATGG	1463
Sbjct 29327	GTCCCTCCCCCTGCAAGAACCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCGAGTCATGG	29386
Query 1464	CTGGAGCCCGTGCAGCTCTCAGGAGCGTCTTCGCCAACAGCCTGGTATGGCGCTCG	1523
Sbjct 29387	CTGGAGCCCGTGCAGCTCTCAGGAGTAGTGTGCCAACACCTGGTATGACACCTCG	29446
Query 1524	GACAGCAACGCTTATGCCAACCTGAAGGAGACCTAGAGGAAGGCATCCAAACGCTGATGG	1583
Sbjct 29447	GACAGCGATGACTATCACCTCTCAAAGGACCTAGAGGAAGGCATCCAAACGCTGATGGG	29506

Query 1584	GTGAGGGTGGCACCA-GGAT--CCAACTCTGGGGCCCCACTGGCTTCCAGGGACT--GGG	1639
Sbjct 29507	GTGAGGGTGGCGCAGGGGTCRCCAATCTGGAAACCCACTGGCTTGAGGG-CTGGGG	29565
Query 1640	AGAGAACACTGCTGCCCTTTAGTCAGTCAGCGCTGACCCAAAGAGAACTCACCGTA	1699
Sbjct 29566	AGAGAACACTGCTGCCCTTTAGTCAGTAAGCGCTGACCCAAAGAGAACTCACCTTA	29625
Query 1700	TTCTTCATTCCTCGTGAATCCTCCAGGCCCTTCTACACCTGGGGGGAGGGAGG	1759
Sbjct 29626	TTCTTCATTCCTCGTGAATCCTCCAGGCCCTTCTACACCTGAAGGGGGAGGGAGG	29685
Query 1760	AAAATGGATGAATGAGAGAGGGAGGAACAGTGCCCAAGCGCTTGGCCCTCCTCTCTT	1819
Sbjct 29686	AAAATGGATRAATGAGAGAGGGAGGGAAACAGTGCCCAAGCGCTTGGCCCTCCTCTCTT	29745
Query 1820	CCTTCACTTGCAGAGGCTGGAAGATGGCAGCCCCGGACTGGCAGATCTCAATCAGT	1879
Sbjct 29746	CCTTCACTTGCAGAGGCTGGAAGACGGCAGCCGGACTGGCAGATCCTCAAGCAGA	29805
Query 1880	CCTACAGCAAGTTGACACAAAATCGCACAAACGATGACGCACTGCTCAAGAACTACGGGC	1939
Sbjct 29806	CCTACAGCAAGTTGACACAAAATCGCACAAACGATGACGCACTGCTCAAGAACTACGGGC	29865
Query 1940	TGCTCTACTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATGTGCAGT	1999
Sbjct 29866	TGCTCTACTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATGTGCAGT	29925
Query 2000	GCCGCTCTGGAGGGCAGTGTGGCTCTAGCTGCCGGGTGGCATCCCTGTGACCCCT	2059
Sbjct 29926	GCCGCTCTGTRGAGGGYAGCTGTGGCTCTAGGTGCCGMTRGCATCC-TGTGACCCCT	29984
Query 2060	CCCCAGTGCCTCTCTGGCTGTTGAAAGGTGCTACTCCAGTGCCTGGCACCAGCCTTGTCTAA	2119
Sbjct 29985	CCCCAGTGCCTCTCTGGCCCTG-AAGGTGCCACTCCAGTGCCTGGCACCAGCCTTGTCTAA	30043
Query 2120	AAAAATTAAAGTTGATCATTTTGTGACTAGGTGTCTTGATATAATTATATGGGTGGA	2179
Sbjct 30044	AAAAATTAAAGTTGATCATTCATCTGACTAGGTGTCTTGATATAATTATATGGGTGGA	30103
Query 2180	-GGCGGGTGGTATGGAGCAAGGGGCCAGGTGGAAAGACA-ACCTGTAGGGCTTCAGGG	2237
Sbjct 30104	AGGTGG-TGGTATGGAGCAAGGGT-AGGT-GGAAAGA-AGACCTGGAGGGCTTCAGG	30159
Query 2238	TCTATTGGAAACCGAGC 2255	
Sbjct 30160	TCTATT-GGGAACCTAGGC 30176	

Score = 1914 bits (1036), Expect = 0.0
 Identities = 1365/1522 (89%), Gaps = 42/1522 (2%)
 Strand=Plus/Plus

Query 765	CAGCTCTGGAACAGGGAGAGCGCTGGCTCTGCTCTCCAGCTCCCTGTG-CCTCC	823
Sbjct 51505	CAGCTCTGGAGCAGGGAGAGCGCTGGCTCTCCAGCTCCCTGTG-CCTCC	51564
Query 824	GGTTCTCCCAAGGCTCCCGAGCTCCCTGCTCTGGCTTTGGCTGCTCGCTGTCC	883

Sbjct	52460	TTCTTCATTCGCCTGGTGAATCCTCCAGGCCYTTCTACACCCCTGAAGGGGAGGGAGG	52519
Query	1760	AAAATGGATGAATGAGAGAGGGAGGGAACAGTGCCTGCCAAGCGCTTGGCCTCTCCTCTT	1819
Sbjct	52520	AAAATGGATGAATGAGAGAGGGAGGGAACAGTGCCTGCCAAGCGCTTGGCCTCTCCTCTT	52579
Query	1820	CCTTCACTTGCAGAGGCTGGAAAGATGGCAGCCCCGGACTGGCAGATCTTCAATCAGT	1879
Sbjct	52580	CCTTCACTTGCAGAGGCTGGAAAGACGGCAGCCGGACTGGCAGATCTTCAAGCAGA	52639
Query	1880	CCTACAGCAAGTTGACACAAAATCGCACACCGATGACGCACTGCTAAGAACTACGGGC	1939
Sbjct	52640	CCTACAGCAAGTTGACACAAAATCRCACAAACCATGACGCAGTGCCTAAGAACTACGGGC	52699
Query	1940	TGCTCTACTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATGTCAGT	1999
Sbjct	52700	TGCTCTACTGCTTCAGGAAGGACATGGACAAGGTCGAGACATTCTGCGCATGTCAGT	52759
Query	2000	GCCGCTCTGTGGAGGGCAGCTGTGGCTCTAGCTGCCGGTGGCATCCCTGTGACC--C	2057
Sbjct	52760	GCCGCTCTGTAGAGGGTAGCTGTGGCTCTAGGTGCCCGTGGCATCC-TGTGACCGAC	52818
Query	2058	C--TCCCCAGTGCCTCTCCTGGTCGTGGAAAGGTGCTACTCCAGTGCCACCAGCCTTGT	2115
Sbjct	52819	CCCTCCCCAGTGCCTCTCCTGGCCCTGGAAAGGTGCCACTCCAGTGCCCATCAGCCTTGT	52878
Query	2116	CTAATAAAATAAGTTGCATCTTGTGGACTAGGTGTCTGTATAATATTATGGG	2175
Sbjct	52879	CTAATAAAATAAGTTGTATCTCATCTGACTAGGTGTCTATCTATAATATTATGGG	52938
Query	2176	TGGA-GGCGGGTGGTATGGAGCAAGGGGCCAGGGTGGAAAGACA-ACCTGTAGGGCCTTC	2233
Sbjct	52939	TGGAAGGTGG-TGGTATGGAGCAAGGGGT-AGGT-GGAAAGA-AGACCTGGAGGGCCTTC	52994
Query	2234	AGGGTCTATTCGGGAACCAGGC	2255
Sbjct	52995	AAGRCTTATT-GGGAACTAGGC	53015

Score = 1879 bits (1017), Expect = 0.0
 Identities = 1359/1522 (89%), Gaps = 48/1522 (3%)
 Strand=Plus/Plus

Query	765	CAGCTCCTGGAACAGGGAGAGCGCTGGCCTTGTCTCCAGCTCCCTGTGTTG-CCTCC	823
Sbjct	13985	CAGCTCCTGGAACAGGGAGAGGTGCTGGCCTTGTCTCCAGCTCCCT-TCTTGCCTCC	14043
Query	824	GGTTCTCCCCCAGGCTCCCGAACGTCCCTGCTCTGGCTTTGGCTCTGCCCTGTCC	883
Sbjct	14044	GGTTCTCCCCCAGGCTCCCGAACGTCCCTGCTCTGGCTTTGGCTCTGCCCTGTCC	14103
Query	884	TGGCTTCAAGAGGGC-AGTGCCTCCAAACCATCCCTTATCCAGGTTTGACA-ACG	941
Sbjct	14104	TGGCTTCAAGA-GGCTGGTCCGTCACCGTCCCTTATCCAGGTTTT-AAAGAGG	14161
Query	942	CTATGCTCCGCCCGTCGC-CTGTACAGCTGG-CATATGACACCTATCAGGAGTTGT	999
Sbjct	14162	CTATGCTCCAAGCCCACGTCGC-ACACCAAGTGGCCAT-TGACACCTACCAGGAGTTAT	14219
Query	1000	AAGCTTGGTAAATGGTGCCTCAGAGGTGGCAGGAAGGGGAGG	1058

Sbjct	14220	::::: ::::: ::::: ::::: ::::: ::::: :::::	14279
Query	1059	GGGAAGTAATGGGAGGAGACTAAGGAGCTCAGGGTTGTTCTGAAGTAAAATGCAGGC	1118
Sbjct	14280	GGGAAGTAATGGGAGGASACTAAGGAGCTCAGGGTTGTTCTGAAGYGAAAATGCAGGC	14339
Query	1119	AGATGAGCATACGGCTGAGTGAGGTTCCCAAGAAAAGTAACAATGGGAGCAGGCTCCAGCA	1178
Sbjct	14340	AGATGAGCATAGGCTGAGCCAGGTTCCCAAGAAGATAACAGTGGGAGCTGGCTCCAGCA	14399
Query	1179	T----AG-A-----C--CTTGGTGGGGCGGTCCTCTCTAGGAAGAAGCCTATATC-CT	1224
Sbjct	14400	TAGAAAGCAGTGGTCCTCTGGTGGGGGCTCTCCCTAGGAAGAAGCCTATATCAC-	14458
Query	1225	GAAGGAGCAGAAGTATTCACTTCTGCAGAACCCCCCAGACCTCCCTCTGCTTCTCAGAGT	1283
Sbjct	14459	AAAGGAACAGAAGTATTCACTTCTGCATG-ACCTCCAGACCTCCCTGCTTCTCAGACT	14517
Query	1284	CTATTCACACA-CCTTCCAAACAGGTGAAAACCGCAGCAGAAATCTGTGAGTGGATGCCT-	1341
Sbjct	14518	CTATTCGACATCC-TCCAACATGGAGGAAACCGCAGCAGAAATCCGTGAGTGGATG-CTG	14575
Query	1342	TCTCCCC-AGG-TGGGATGGGGTAGACCTGTGGTCAGAGCCCCCGGGCAGCACAGCCACT	1399
Sbjct	14576	TCTCCCCTAGGGGGATGGGGAGACCTGTGGTCAGAGCCCCCGGGCAGCACAGCCACT	14635
Query	1400	GCCGGTCCTTCCCCCTGCAGAACCTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTC	1459
Sbjct	14636	GCCGGTCCTTCCCCCTGCAGAACCTAGAGCTGCTCCACATCTCCCTGCTGCTCATCGAGTC	14695
Query	1460	ATGGCTGGAGCCCGTGCAGCTCTCAGGAGCGCTTCGCCAACAGCTGGTGTATGGCG	1519
Sbjct	14696	CGGGCTGGAGCCCGTGCAGCTCTCAGGAGTACCTTCAACAAACCTGGTGTATGACAC	14755
Query	1520	CTCGGACAGAACGTCTATGCCACCTGAAGGACCTAGAGGAAGGCATCCAAACGCTGAT	1579
Sbjct	14756	CTCGGACAGYGTGAMTATCACCTCTAAAGGACCTAGAGGAAGGCATCCAAATGCTGAT	14815
Query	1580	GTGGGTGAGGGTGGCACCA-GGAT--CCAATCCCTGGG-GCCCCACTGGCTTCCAGGGACT	1635
Sbjct	14816	GGGGGTGAGGGTGGCACCGAGGGTCCCCAATCTGGAAAGGCC-ACTGGCTTCGAGGG-CT	14873
Query	1636	GGGG-AGAAACACTGCTGCCCTTTTAGCAGTCAGGCCCTGACCCAAGAGAACTCA	1694
Sbjct	14874	GGGGAGAGAAACACTGCTGCCCTTTAGCAGTCAGGCCCTGACCCAAGAGAACTCA	14933
Query	1695	CCGTATTCTCATTTCCCCTCGTAATCCTCCAGGCTTCTCTACAACCTGGGGGAG	1754
Sbjct	14934	CCWTATTCTCATTTCCCCTCGTAATCCTCCAGGCTTCTCTACACCCCTGRAGGGGAA	14993
Query	1755	GGAGGAAAATGGATGAATGAGAGAGGGAGGGAAACAGTGCCTGGCTCTCCCTT	1814
Sbjct	14994	GGAGGAAAATGGATAATGAGAGAGGGAGGGAAACAGTGCCTGGCTCTCCCTT	15053
Query	1815	CTCTTCTTCACTTGAGAGGCTGGAAGATGGCAGCCCCGACTGGCAGATCTCAA	1874
Sbjct	15054	CTCTTCTTCACTTGAGAGGCTGGAAGACGGCAGCCACCTGACTGGCAGACCCCAA	15113
Query	1875	TCAGTCCCTACAGCAAGTTGACACAAAATCGCACAAACGATGACGGCACTGCTCAAGAACTA	1934

Sbjct	15114	GCAGACCTACAGCAAGTTGACACAAACTCGCACAACCATGACGCACTGCTCAAGAACTA	15173
Query	1935	CGGGCTGCTCTACTGCTTCAGGAAGGCACATGGACAAGGTCGAGACATTCTCGGCATCGT	1994
Sbjct	15174	CGGGCTGCTCCACTGCTTCAGGAAGGCACATGGACAAGGTCGAGACATTCTCGGCATGGT	15233
Query	1995	GCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTCTAGCTGCCCCGGTGGCATCCCTGTGA	2054
Sbjct	15234	GCAGTGCCGCTCTGTGGAGGGCAGCTGTGGCTCTAGGGGCCGCGTGGCATCC-TGTGTA	15292
Query	2055	CCCCCTCCCAGTGCTCTCCCTGGCTGTGGAGGTGCTACTCCAGTGCCCCACAGCCTGT	2114
Sbjct	15293	CCYCTCCCCAGTGCTCTCCCTGGCCCTG-AAGGTGCCACTCCAGTGCCCCACAGCCTGT	15351
Query	2115	CCTAATAAAATTAAAGTGTGATCATTTGTTGACTAGGTGTCCTTGATAATAATTATGGG	2174
Sbjct	15352	CCTAATAAAATTAAAGTGTATTGTTGACTAGGTGTCCTTGATAATAATTATGGG	15411
Query	2175	GTGGA-GCCGGGTGGTATGGAGCAAGGGGCCAGGTTGGAAAGACAACCTGTAGGGCCTTC	2233
Sbjct	15412	GTGGAAGGTGG-TGGTATGGAGCAAGGGGT-AGGT-GGRAAGACGACTGGAGGGCCTTC	15468
Query	2234	AGGGTCTATTGGAAACAGGC 2255	
Sbjct	15469	AGGGTCTATT-GGGAACTAGGC 15489	

Score = 1081 bits (585), Expect = 0.0
Identities = 688/737 (93%), Gaps = 11/737 (1%)
Strand=Plus/Plus

Query	1	GAATT CAG CACT GAAT CATGCCAGAACCCCCGCAATCTATTGGCTGTGCCTTGGCCCT	60
Sbjct	13231	GAATT CAG GACT GAAT CATGCTCACACCCCCAACATCTATTGGCTGTGC- TTGGCCCT	13289
Query	61	TTTCCCAACACACACATTCTGCTGGTGGGGAGGGGAAACATGCGGGGAGGAGGAAAG	120
Sbjct	13290	TTTCCCAACACACACATCTGCTGGTGGGGAGGTTAACATGCGGGGAGGAGGAAAG	13349
Query	121	GAATAGGATAGAGAGTGTTGGATGGGGTCTGGTGGGGTCTCAAGGACTGCCCTATCTGACA	180
Sbjct	13350	GAATAGGATAGAGAGTGTTGGATGTGGTCTGATGGGGTCTCAAGGACTGG-CTATCTGACA	13408
Query	181	TCCCTTCGCCGTTCAAGTTGGCCACCATGGCCTGCTGCCAGAGGGCACCCACGTGACCC	240
Sbjct	13409	TCCCTTCCKCATTCAAGTTGGCCACCATGGCCTGCTGCCAGAGGGCACCCACCTGAACC	13468
Query	241	TTAAAGAGAGGACAAGTTGGTGGTATCTCTGGCTGACATTCTGTGCACAACCCCTACAA	300
Sbjct	13469	TTAAAGAGAGGACAAGTTGGTGGTCTGTGGTGCACACTCTGTGCACAACCCCTACAA	13528
Query	301	CGCTGGTGATGGTGGGAAGGGAAAGATGACAAGTCAGGGGCATGATCCAGCATGTGTG	360
Sbjct	13529	CGCTGGTGACGGTGGGAAGGGAAAGATGACAAGCCAGGGGCATGATGCCAGCATGTGTG	13588
Query	361	GGAGGAGCTCTCAAATTATCCATTAGCACAAGCCCGTCAGTGGCCCTAACATG	420
Sbjct	13589	GGAGGAGCTCTCAAATTATCCATTAGCACAAGCCCGTCAGTGGCCCTAACATG	13648

Query	421	CAGAGAACAGGTGAGGAG-AAGCAGCGAGAGAGAAGGGGCCAGG-TATAAAAAGGGCCC	478
Sbjct	13649		13706
Query	479	ACAAGAGACCAAGCTCAAGGATCCCAAGGCCAACTCCCGAACCACTCAGGGTCTGTGG	538
Sbjct	13707	ACAAGAGACCAAGCTCCAGCATCCCAAGGCCAACTCCCGAACCACTCAGGGTCTGTGG	13766
Query	539	ACAGCTCAC-TAGCGGAATGGCTGCAGGTAAGCGCCCCCTAAATCCCTTGG-CACAAT	596
Sbjct	13767		13826
Query	597	GTGTCCTGAGGGGGAGAGGCCGCCTGCTGTAGATGGACGGGGGCACTAACCTCAGGTT	656
Sbjct	13827	GTGTCCTGAGGGGGAGAGGCCGCCTGCTGTAGATGGACGGGGGCACTAACCTCAGGTT	13885
Query	657	GGGGCTTATGAATGTTAGCTATGCCATCTAACGCCAG-TATTTGGCAATCTCTGAATG	715
Sbjct	13886		13944
Query	716	TTCTGGTCCCTGGAGG 732	
Sbjct	13945	TTCTGGTCCCTGGAGG 13961	

Score = 1068 bits (578), Expect = 0.0
Identities = 677/736 (91%), Gaps = 8/736 (1%)
Strand=Plus/Plus

Query	1	GAATTTCAGCACTGAATCATGCCAGAACCCCCGCAATCTATTGGCTGTGCTTGGCCCC	60
Sbjct	5660	GAATTCAAGACTGAATCGTCTCACACCCCCAACATCTATTGGCTGTGC-TTGGCCCC	5718
Query	61	TTTCCCAACACACACATTCTGTCTGGTGGGGAGGGAAACATGCGGGGAGGAGGAAG	120
Sbjct	5719	TTTCCCAACACACACATTCTGTCTGGTGGGGAGGGAAACATGCGGGGAGGAGGAAG	5778
Query	121	GAATAGGATAGAGAGTGGGATGGGTCTGTA-GGGGTCTCAAGGACTGGCCTATCCTGAC	179
Sbjct	5779	GRATAGGATAGAGARTGGGATGKGGTCGGTAGGGGTCTCAAGGACTGG-CTATCCTGAC	5837
Query	180	ATCCTTCTCCGCGTTCAGGTGGCCACCATGGCTGCTGCCAGAGGGCACCCACGTCACC	239
Sbjct	5838	ATCCTTCKCCGCGTKCAGGTGGCCACCATGGCTGCDGCCAGAGGGCACCCACSTGACC	5897
Query	240	CTTAAAGAGAGGACAAGTTGGGTGTTATCTCTGGCTGACATTCTGTGCAACCCCTCACA	299
Sbjct	5898	CTTAAAGAGAGGACAAGTTGGGTGTTATCTCTGGCTGACACTCTGTGCAACCCCTCACA	5957
Query	300	ACGCTGGTGTGGTGGGAAAGGAAAGATGACAAGTCAGGGGCATGATCCCACATGTGT	359
Sbjct	5958	ACACTGGTACGGTGGGAAAGGAAAGAYGACAAGCCAGGGRCATGATSCCAGCATGTGT	6017
Query	360	GGGAGGAGCTTCTAAATTATCATTAGCACAAGCCCGTCAGTGGCCCCAGGCCAAACAT	419
Sbjct	6018	GGGAGGAGCTTCTAAATTATCATTAGCACAAGCCCGTCAGTGGCCCCATGCATAATGT	6077
Query	420	GCAGAGAAACAGGTGAGGAGAACGAGCAGCAGAGAGAGGGGCCAGG-TATAAAAGGGCCC	478
Sbjct	6078	RCACAGAAAACAGGTGGGKCAA-CAGTGGGAGAGAACGGGCCAGGTATAAAAGGGCCC	6136

Query	479	ACAAAGAGACCAGCTCAAGGATCCAAGGGCCAACCTCCCGAACCCACTCAGGGTCTGTGG	538
Sbjct	6137	ACAAAGAGACCAGCTCAAGGATCCAAGGGCCAACCTCCCGAACCCACTCAGGGTCTGTGG	6196
Query	539	ACAGCTCAC-TAGCGGCAATGGCTCGAGGTAAGGCCCTAAATCCCTTG-CACAAT	596
Sbjct	6197	ACAGCTCACCTAGCGBCAATGGCTCAGGTAAGGCCCTAAATCCCTTG-GGACAAY	6256
Query	597	GTGTCTGAGGGGAGAGCGCGCTCTGTAGATGGGACGGGGCACTAACCTCAGGTT	656
Sbjct	6257	GTGTCTGAGGGGAGAGCGAGCTGTAGATGGGACGGGGCACTAACCTCAGGTT	6316
Query	657	GGGGCTTATGAATGTTAGCTATGCCATCAAGCCAGTATTTGCCAATCTCTGAATGT	716
Sbjct	6317	GGGGCTTCTGAATGTGAG-TATGCCATSTAAGCCAGTATTCGKCCAACTCAGAAAGC	6375
Query	717	TCCTGGTCCCTGGAGG 732	
Sbjct	6376	TCCTGGTCCCTGGAGG 6391	
 Score = 1037 bits (561), Expect = 0.0			
Identities = 680/737 (92%), Gaps = 9/737 (1%)			
Strand=Plus/Plus			
Query	1	GAATTCAAGCACTGAATCATGCCAGAACCCCCGCAATCTATTGGCTGTGCCTTGGCCCT	60
Sbjct	27913	GAATTCAAGCACTCAATGGCTCAGAACCCCCAACATCTATTGGCTGTGC-TTGGCCCT	27971
Query	61	TTTCCCACACACACATTCTGTCTGGTGGGAGGGAAACATCGGGAGGGAGGAAAG	120
Sbjct	27972	TTTCCCACACACACATTCTGTCTGGTGGGAGGTTAACACGGGGAGGGAGGAAAG	28031
Query	121	GAATAGGATAGAGAGTGGGATGGGTCGGTAGGGGCTCAAGGACTGGCTATCTGACA	180
Sbjct	28032	GAATAGGATAGAGAGTGGGAATGGGTCGGTAGGGGCTCAAGGACTGG-CTATCTGACA	28090
Query	181	TCCTTCTCCCGCTCAGGGTGGGCCACCATGGCCTGCTGCCAGAGGGCACCCACGTGACCC	240
Sbjct	28091	GCCTTCCCCCGCTCAGGGTGGACCAACATGGCCTGCGACCCAGAGGGCACCCACGTGACCC	28150
Query	241	TTAAAGAGAGGACAAGTTGGGTGTA-TCTCTGGCTGACATCTGTGACAAACCTCACA	299
Sbjct	28151	TTAAAGAGAGGACAAGTTGGGTGG-AGTCCTGGCTGACACTCTGTGACAAACCTTACA	28209
Query	300	ACGCTGGTGTGGGGAAAGGGAAAGATGACAAGTCAAGGCGATGATCCCAGCATGT	359
Sbjct	28210	ACACTGGTGTGGTGGAGAAGGGAAAGACGACAAGCCAGGGGCGATGATCCCAGCATGT	28269
Query	360	GGGAGGAGCTCTAAATTATCATTAGCACAGCCGTCACTGGCCCCAGGCCAAACAT	419
Sbjct	28270	GGGAGGAGCTCTAAATTATCATTAGCACAGCCGTCACTGGCCCCAGGCCAAACAT	28329
Query	420	GCAGAGAAAAGGGTGGAGGAGAACGAGCGAGAGAGAAGGGGCCAGG-TATAAAAGGCC	478
Sbjct	28330	ACACAGAAAAGGGTGGGTCAAGCAGGGAGAGAGAACTGGCCAGGGTATAAAAGGCC	28389
Query	479	AACAGAGACCAGCTCAAGGATCCAAGGCCAACCTCCCGAACCCACTCAGGGTCTGTGG	538

Sbjct	28390	ACAAGAGACCGGCTAGGATCCAAGGCCAACTCCCGAACCACTCAGGGTCCTGTGG	28449
Query	539	ACAGCTCAC-TAGCGGCAATGGCTGCAGGTAAGCGCCCTAAATCCCTTG-CACAAT	596
Sbjct	28450	ACAGCTCACCTAGTGGCAATGGCTCAGGTAAGGCCCTAAATCCCTTG-GGCCACAAC	28509
Query	597	GTGTCTGAGGGGAGAGGCAGCGCCCTGTAGATGGGACGGGGCACTAACCTCAGGTT	656
Sbjct	28510	GTGTCTGAGGGGAGAGGCAGCGCCCTGTAGATGGGACGGGGCACTAACCTCAGGTT	28569
Query	657	GGGGCTTATGAATGTTAGCTATGCCATCTAACGCCAG-TATTGGCCAATCTGAATG	715
Sbjct	28570	GGGGCTTATGAATGTTAGCTATGCCATCTAACGCCAGATTTGGCCAATCTGAATG	28628
Query	716	TCCTGGTCCCTGGAGG 732	
Sbjct	28629	TCCTGGTCTCTGGAGG 28645	

Score = 1037 bits (561), Expect = 0.0
 Identities = 680/737 (92%), Gaps = 9/737 (1%)
 Strand=Plus/Plus

Query	1	GAATTCACTGAATCATGCCAGAACCCCCCAATCTATTGGCTGTGTTGGCCCT	60
Sbjct	50747	GAATTCACTGAATGGTCTCAGAACCCCCAACATCTATTGGCTGTGC-TTGGCCCT	50805
Query	61	TTCCCAACACACACATTCTGCTGGGGGGAGGGAAACATGCGGGGAGGAGGAAAG	120
Sbjct	50806	TTCCCAACACACACATTCTGCTGGGGGGAGGTTAACACCGCGGGGAGGAGGAAAG	50865
Query	121	GAATAGGATAGAGTGGATGGGTCTCGTAGGGCTCAAGGACTGGCTATCTGACA	180
Sbjct	50866	GAATAGGATAGAGTGGATGGGTCTCGTAGGGCTCAAGGACTGG-CTATCTGACA	50924
Query	181	TCCTCTCCCGCTCAGGTGGCACCATGGCTGCTGCCAGAGGGCACCCACGTGACCC	240
Sbjct	50925	GCCTTCCCCCGCTCAGGTGACCAACATGGCTGCGAGCCAGAGGGCACCCACCTGACCC	50984
Query	241	TTAAAGAGAGGACAAGTTGGGTGTA-TCTCTGGCTGACATTCTGTGCAACACCCCTACA	299
Sbjct	50985	TTAAAGAGAGGACAAGTTGGGTGG-AGTCTGTGGCTGACACTCTGTGACAATCCTTACA	51043
Query	300	ACGCTGGTATGGTGGGAAGGAAAGATGACAAGTCAGGGGCATGATCCAGCATGTGT	359
Sbjct	51044	ACACTGGTATGGTGGAGAAGGGAAAGACGACAAGCCAGGGGCATGATCCAGCATGTGT	51103
Query	360	GGGAGGAGCTCTAAATTATCATTAGCACAAGCCGTCACTGGCCAGGCCAACAT	419
Sbjct	51104	GGGAGGAGCTCCAAATTATCATTAGCACAAGCCGTCACTGGCCAGGCCAACAT	51163
Query	420	GCAGAGAAAACAGGTGAGGAGAACGAGCAGGAGAGAAGGGGCCAGG-TATAAAAGGGCCC	478
Sbjct	51164	ACACAGAAAACAGGTGGGTCAAGCAGGGAGAGAGAACCTGGCAGGGTATAAAAGGGCCC	51223
Query	479	ACAAGAGACCACTCAAGGATCCAAGGCCAACTCCCGAACCACTCAGGGTCCTGTGG	538
Sbjct	51224	ACAAGAGACCGGCTAGGATCCAAGGCCAACTCCCGAACCACTCAGGGTCCTGTGG	51283
Query	539	ACAGCTCAC-TAGCGGCAATGGCTGCAGGTAAGGCCCTAAATCCCTTG-CACAAT	596

Sbjct	51284	ACAGCTCACCTAGTGGCAATGGCTCCAGGTAGCGCCCCCTAAAATCCTTGGGCACAAAC	51343
Query	597	GTGTCCCTGAGGGGGAGAGGCCGCGTCCTGTAGATGGGACGGGGGCACTAACCCTCAGGTT	656
Sbjct	51344	GTGTCCCTGAGGGAGAGGCCGCGCCCTGTAGATGGGACGGGGGCACTAACCCTCAGGTT	51403
Query	657	GGGGCTTATGAATGTAGCTATGCCATCTAACGCCAG-TATTGGCCAATCTCTGAATG	715
Sbjct	51404	GGGGCTTATGAATGTGAG-TATGCCATCTAACGCCAGATTTGGCCAATCTCTGAATG	51462
Query	716	TTCCCTGGTCCCTGGAGG 732	
Sbjct	51463	TTCCCTGGTCCCTGGAGG 51479	

Score = 545 bits (295), Expect = 6e-152
Identities = 376/415 (90%), Gaps = 5/415 (1%)
Strand=Plus/Plus

Query	2250	CCAGGGCTGGAGTCAGTGGCA-G-TCTTGGCTCGCTGCAATCTCCGCCTCTGGGTCAA	2307
Sbjct	574	CCAGGGCTAGAGTCATGGCACGATCTGGCTCACTGACCCCTCACCTCTGGGTCAA	633
Query	2308	GCGATTCTCTGCCTCAGTCTCCGAA-TAGTTGCGATTCCAGGCATGCAAGGACAGGCT	2366
Sbjct	634	GCGATTCTCTGCCTCAGCCTCTC-AAGTAGCTGGATTACAAGGCCTACACCAGGCT	692
Query	2367	CAGCTAATTCTGTATTTGGTAGAGACGGGGTTTACCATATTGGCCAGTCTGGCTC	2426
Sbjct	693	CCGCTAATTCTGTATTTAGTAGAGACGGGGTTTACCATATTGGCCAGGCTGGCTC	752
Query	2427	CATCTCCTGACCTCAGGTAACTCCGCCGCGCTCGGCCTCCCAAATTGCTGGGATTACAGGT	2486
Sbjct	753	CAACTCTGACCTCAGGTGATCCGCCGCCCTGGCCTCCCAAATTGCTGGGATCACAGAT	812
Query	2487	ATGAGGCCACTGGGCCCTCCCTGTCTT-GTAGTTAAAATAATTATACCGCAGAAGGAA	2545
Sbjct	813	GTAAGCCACTGCGCCCTCCCTGTCTTGTCAATTAAAATAATTATACCGCAGGAGGA	872
Query	2546	CGTCAGACACAGCATGGGTACCTGGCATGCCAGGCCAGTGGACATTGAGTTGTTT	2605
Sbjct	873	CGTCAGACACAGCATGGGTACCTGGCATGCCAGGCCAGTGGGACATTGAGTTCTTT	932
Query	2606	GCTTGGCACTGTCTCTCATGCATTGGTCCACTCAGTAGATGCTGGAAITC	2660
Sbjct	933	GCTTGGCACTGTCTCTCATGCATTGGTCCACTCAGTAGATGCTTATTGAAITC	987

Score = 209 bits (113), Expect = 8e-51
Identities = 213/260 (81%), Gaps = 12/260 (4%)
Strand=Plus/Plus

Query	2365	CTCAGCTAATTTGTATTTT-GGTAGAGACGGGGTTCACCATATTGCCAGTCGGT	2423
Sbjct	41767	CCCAGCTAATTTGTATTTAGG-AGAGATGGAGTTGCCATGTGGGTTAGCCTGGT	41825
Query	2424	CTC-CATCTCTGACCTCAGGTATCCGCCGCCCTCGGCCCTCCAAATTGCTGGGATTAC	2482
Sbjct	41826	CTTGCA-CTCCIGACCTTAAGTGTATCCACCCACCTCAGCCTCCAAAGTGTGGGATTAT	4184
Query	2483	AGGTATGAGCCACTGGCCC 2502	
Sbjct	41885	AGGCATGAGCCACCGTGCCC 41904	

>gb|GC699295.1| Sequence 14540 from patent US 6812339
Length=5692

Score = 2802 bits (1517), Expect = 0.0
Identities = 1780/1907 (93%), Gaps = 17/1907 (0%)
Strand=Plus/Plus

Query	765	CAGCTCTGGAACAGGGAGAGCGCTGGCCTCTGCTCTCCAGCTCCCTGTGTTG-CCTCC	823
Sbjct	2313	CAGCTCTGGAGCAGGGAGAGTGCTGGCCTCTGCTCTCCGGCTCCCTGTGTTGCCCTCT	2372
Query	824	GGTTTCTCCCCAGGCTCCGGAGCTGGCCTCTGCTCTGGCTTTGGCTGCTCTGCCCTGTC	883
Sbjct	2373	GGTTTCTCCCCAGGCTCCGGAGCTGGCCTCTGCTCTGGCTTTGGCTGCTCTGCCCTGCCC	2432
Query	884	TGGCTCAAGAGGGCAGTGCCCTCCAACCATCCCTTATCCAGGCTTTGACAACGCT	943
Sbjct	2433	TGGCTCAAGAGGGCAGTGCCCTCCAACCATCCCTTATCCAGGCTTTGACAACGCT	2492
Query	944	ATGCTCCGCGCCCGTCGCCCTGACAGCTGGCATATGACACCTATCAGGAGTTGTAAGC	1003
Sbjct	2493	ATGCTCCGCGCCCATCGCTCTGCACCAGCTGGCCTTGACACCTACCCAGGAGTTGTAAGC	2552
Query	1004	TCTTGGGTAATGGGTGCGCTTCAGGGTGGCAGGAAGGGGTGAATTCCCCCGCTGGAA	1063
Sbjct	2553	TCTTGGGATGGGTGCGCATCAGGGTGGCAGGAAGGGGTACTTCCCCCGCTGGAA	2612
Query	1064	GTAATG-GGAGGGAGACTAAGGAGCTCAGGGTTGTTCTGAAGTGAAAATGCAGGCAGAT	1122
Sbjct	2613	ATAA-GGAGGAGGAGACTAAGGAGCTCAGGGTT-TTCCGAAGCAGAAATGCAGGCAGAT	2670
Query	1123	GAGCATACGCTGAGTGAGGTTCCAGAAAAGTAACAATGGGAGCAGGTCTCCAGCATAGA	1182
Sbjct	2671	GAGCACACGCTGAGTGAGGTTCCAGAAAAGTAACAATGGGAGCTGGTCTCCAGCGTAGA	2730
Query	1183	CCTTGGTGGGGCGGTCTCTCTAGGAAGAAGCCTATATCCTGAAGGAGCAGAAGTATT	1242
Sbjct	2731	CCTTGGTGGGGCGGTCTCTCTAGGAAGAAGCCTATATCCAAAGGAACAGAAAGTATT	2790
Query	1243	ATTCTGCAAGAACCCCCAGACCTCCCTGCTTCTCAGAGTCTATTCCAACACCTCCAA	1302
Sbjct	2791	ATTCTGCAAGAACCCCCAGACCTCCCTGTTCTCAGAGTCTATTCCGACACCTCCAA	2850
Query	1303	CAGGGTGAACACGCAAGAAATCTGTGAGTGGATGCCCTCCCGAGG-TGGGATGGGG	1361
Sbjct	2851	CAGGGAGGAACACAAACAGAAATCCGTGAGTGGATGCCCTCTCCCAAGGCGGGGATGGG	2910

Query 1362	TAGACCTGTGGTCAGAGCCCCGGGCAGCACAGCCACTGCCGGTCCCTCCCTGCAGAAC	1421
Sbjct 2911		2970
Query 1422	CTAGAGCTGCTCCGCATCTCCCTGCTGCTCATCCAGTCATGGCTGGAGGCCGTGCAGCTC	1481
Sbjct 2971		3030
Query 1482	CTCAGGAGCGCTTCGCAAACAGCCTGGTGTATGGCCTCGGCCAGCAACAGTCTATCG-	1540
Sbjct 3031		3089
Query 1541	CCACACTGAAGGACCTAGAGGAAGGCATCCAAACCGCTGATGTGGGTGAGGGTGGCACCA-G	1599
Sbjct 3090		3149
Query 1600	GAT--CCAATCCTGGGGCCCCACTGGCTCCAGGGACTG-GGGAGAGAAACACTGCTGCC	1656
Sbjct 3150		3208
Query 1657	CTCTTTTAGCAGTCAGGCCTGACCCAAGAGAACTCACCGTATTCTCATTTCCCTCG	1716
Sbjct 3209		3268
Query 1717	TGAAATCCTCAGGCCTTCTCTAACACCTGGAGGGAGGGAGGAAATGGATGAATGAGA	1776
Sbjct 3269		3328
Query 1777	GAGGGAGGGAACAGTGCCCAAGCGCTTGGCCTCTCTCTCTTCACTTTGAGG	1836
Sbjct 3329		3388
Query 1837	CTGGAAGATGGCAGCCCCCGGACTGGCAGATCTTCAATCAGTCCTACAGCAAGTTGAC	1896
Sbjct 3389		3448
Query 1897	ACAAAATCGCACACAGATGACGCACTGCTCAAGAACTACGGGTGCTACTGCTTCAGG	1956
Sbjct 3449		3508
Query 1957	AAGGGACATGGACAAGGTGAGACATTCTGCGCATCGTCAGTGGCGCTCTGGAGGGC	2016
Sbjct 3509		3568
Query 2017	AGCTGTGGCTTCTAGCTGCCGGTGGCATCCCTGTGACCCCTCCCAGTGCCTCTCTG	2076
Sbjct 3569		3628
Query 2077	GTCGTGGAAGGTGCTACTCCAGTGCCACCAGCTTGTCTAATAAAATTAAGTGCATC	2136
Sbjct 3629		3688
Query 2137	ATTTGTGACTAGGTGCTTGTATAATATTATGGGGTGGAGGGGGTGGTATGGAGC	2196
Sbjct 3689		3748
Query 2197	AAGGGGCCAGGGGGAGACAACCTGTAGGGCCTCAGGGTCTATTGGGAACCAGGCT	2256
Sbjct 3749		3806

Query 2257	GGAGTGCAGTGGCAG--TCTTGGCTCGCTGCAATCTCCGCCCTCTGGGTCAAGCGATT	2314
Sbjct 3807	GGAGTGCAGTGGCACAATCTGGCTACTGCAATCTCCGCCCTCTGGGTCAAGCGATT	3866
Query 2315	TCTTGCTCAGTCTCCGAATAAGTTCGATTCCAGGCATGCAAGACCAGGCTCAGCTAAT	2374
Sbjct 3867	TCTTGCTCAGCCTCCGAGTTGGATTCAGGCATGCAATGCCAGGCTCAGCTAAT	3926
Query 2375	TTTGTATTTGGTAGAGACGGGTTTACCATATTGGCAGTCGGTCTCCATCTCT	2434
Sbjct 3927	TTTGTTTGGTAGAGACGGGTTTACCATATTGGCAGGCTGGTCTCCAATCT	3986
Query 2435	GACCTCAGGTAACTCGCCCGCTCGGCCCTCCAAATTGCTGGGATTACAGGTATGACCA	2494
Sbjct 3987	AATCTCAGGTGATCTACCCACCTTGGCTCCAAATTGCTGGGATTACAGGCGTGAACCA	4046
Query 2495	CTGGGCCCTTCCCTGTCTG-TGATTTAAATAATTACCAACAGCAGAAGGACGTCCAGA	2553
Sbjct 4047	CTGCTCCCTTCCCTGTCTGATTTAAATAACTACCAACAGCAGGAGGACGTCCAGA	4106
Query 2554	CACAGCATGGGCATCTGGCCATGCCAGCCAGTGGACATTGAGTTGGTCTGGCA	2613
Sbjct 4107	CACAGCATAGGCATACCTGGCCATGCCAACCGTGGGACATTGAGTTGGTCTGGCA	4166
Query 2614	CTGTCTCTCATGCATTGGGCCACTCAGTAGATGCTTGTGAATT	2660
Sbjct 4167	CTGTCTCTCATGCCTGGGCCACTCAGTAGATGCCCTGTTGAATT	4213

Database: Nucleotide sequences derived from the Patent division of GenBank

Posted date: Mar 1, 2009 2:34 AM

Number of letters in database: 537,266,521

Number of sequences in database: 8,753,385

Lambda K H
1.33 0.621 1.12

Gapped

Lambda K H
1.28 0.460 0.850

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 0, Extension: 0

Number of Sequences: 8753385

Number of Hits to DB: 1394086

Number of extensions: 628

Number of successful extensions: 628

Number of sequences better than 10: 419

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 603

Number of HSP's successfully gapped: 603

Length of query: 2660

Length of database: 4832233817

Length adjustment: 32

Effective length of query: 2628

Effective length of database: 4552125497

Effective search space: 11962985806116

Effective search space used: 11962985806116

A: 0

X1: 12 (23.1 bits)

X2: 32 (59.1 bits)
X3: 54 (99.7 bits)
S1: 12 (23.3 bits)
S2: 22 (41.7 bits)